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OM protein - protein search, using sw model

Run on: November 1, 2001, 16:24:05 ; Search time 12.69 seconds
(without alignments)
196.837 Million cell updates/sec

Title: US-09-652-345-6

Perfect score: 543

Sequence: 1 ILLVSDDEHGRAAKRLLET.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	540	99.4	920	1	US-08-026-138E-9
2	540	99.4	920	1	US-08-026-138E-10
3	538	99.1	922	2	US-08-231-193A-14
4	538	99.1	922	2	US-08-231-193A-20
5	538	99.1	922	2	US-08-486-273A-14
6	538	99.1	922	2	US-08-486-273A-20
7	538	99.1	922	3	US-08-480-474-14
8	538	99.1	922	3	US-08-480-474-20
9	538	99.1	922	3	US-08-940-086A-14
10	538	99.1	922	3	US-08-940-086A-20
11	538	99.1	938	2	US-08-231-193A-2
12	538	99.1	938	2	US-08-486-273A-2
13	538	99.1	938	3	US-08-480-474-2
14	538	99.1	938	3	US-08-940-086A-2
15	538	99.1	976	2	US-08-231-193A-22
16	538	99.1	976	2	US-08-486-273A-22
17	538	99.1	976	3	US-08-480-474-22
18	538	99.1	976	3	US-08-940-086A-22
19	532	98.0	863	4	US-08-436-332B-2
20	517.5	95.3	943	2	US-08-231-193A-36
21	517.5	95.3	943	2	US-08-486-273A-36
22	517.5	95.3	943	3	US-08-480-474-36
23	517.5	95.3	943	3	US-08-940-086A-36
24	517.5	95.3	959	2	US-08-231-193A-24
25	517.5	95.3	959	2	US-08-486-273A-24
26	517.5	95.3	959	3	US-08-480-474-24
27	517.5	95.3	959	3	US-08-940-086A-24

28	517.5	95.3	997	2	US-08-231-193A-38	Sequence 38, Appl
29	517.5	95.3	997	2	US-08-486-273A-38	Sequence 38, Appl
30	517.5	95.3	997	3	US-08-480-474-38	Sequence 38, Appl
31	517.5	95.3	997	3	US-08-940-086A-38	Sequence 38, Appl
32	400	73.7	854	2	US-08-231-193A-32	Sequence 32, Appl
33	400	73.7	854	2	US-08-486-273A-32	Sequence 32, Appl
34	400	73.7	854	3	US-08-480-474-32	Sequence 32, Appl
35	400	73.7	854	3	US-08-940-086A-32	Sequence 32, Appl
36	400	73.7	870	2	US-08-231-193A-30	Sequence 30, Appl
37	400	73.7	870	2	US-08-486-273A-30	Sequence 30, Appl
38	400	73.7	870	3	US-08-480-474-30	Sequence 30, Appl
39	400	73.7	870	3	US-08-940-086A-30	Sequence 30, Appl
40	400	73.7	908	2	US-08-231-193A-34	Sequence 34, Appl
41	400	73.7	908	2	US-08-486-273A-34	Sequence 34, Appl
42	400	73.7	908	3	US-08-480-474-34	Sequence 34, Appl
43	400	73.7	908	3	US-08-940-086A-34	Sequence 34, Appl
44	379.5	69.9	777	2	US-08-231-193A-16	Sequence 16, Appl
45	379.5	69.9	777	2	US-08-486-273A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-026-138E-9
; Sequence 9, Application US/08026138E
; Patent No. 5502166
; GENERAL INFORMATION:
; APPLICANT: Masayoshi MISHINA
; TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nishiohata Residence 1-107
; STREET: 5214, Nishiohata-shi
; CITY: Niigata-shi
; STATE: Niigata-ken
; COUNTRY: JAPAN
; ZIP: 951
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS v.5
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,138E
; FILING DATE: 26-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 39563/1992
; FILING DATE: 26-FEB-1992
; APPLICATION NUMBER: JP 173155/1992
; FILING DATE: 30-JUN-1992
; APPLICATION NUMBER: JP 215017/1992
; FILING DATE: 12-AUG-1992
; APPLICATION NUMBER: JP 303878/1992
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamburg, C.Bruce
; REGISTRATION NUMBER: 22,389
; REFERENCE/DOCKET NUMBER: F-4551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-2340
; TELEFAX: (212) 953-7733
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 920 amino acids
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: mouse
; TISSUE TYPE: brain
; PUBLICATION INFORMATION:

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; AUTHORS: Masayoshi MISHINA
;
; .TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
; RELEVANT RESIDUES IN SEQ ID NO: 9: FROM 1 to 920
US-08-026-138E-9

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	Query_Match	99.4%	Score 540;	DB 1;	Length 920;
	Best Local Similarity	99.1%	Pred. No. 3.4e-57;		
	Matches 110;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps
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DB	145	I I I L V S D D H E G R A A Q K R L E T L L E E R S K A E K V I Q F D P G T K N V T A L M E A R D L E A R V I I L S	204		
QY	61	A S E D D A A T V Y R A A A M L N M T G S Y V W L V G E R I S G N A L R Y A P D C G I I G L Q I N	111		
DB	205	A S E D D A A T V Y R A A A M L N M T G S Y V W L V G E R I S G N A L R Y A P D C G I I G L Q I N	255		

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2
US-08-026-138E-10
; Sequence 10, Application US/08026138E
; Patent No. 5502166
; GENERAL INFORMATION:
; APPLICANT: Masayoshi MISHINA
; TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nishiohata Residence 1-107
; STREET: 5214, Nishiohata-machi
; CITY: Niigata-shi
; STATE: Niigata-ken
; COUNTRY: JAPAN
; ZIP: 951
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS v.5
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,138E
; FILING DATE: 26-FEB-1993

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PRIOR APPLICATION DATA: JP 30563/1992
FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-4551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 986-2340
TELEFAX: (212) 953-7733
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 amino acids
TYPE: amino acid
STRANDEDNESS: single strand
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: mouse
TISSUE TYPE: brain
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CO-
RELEVANT RESIDUES IN SEQ ID NO: 10
US-08-026-138B-10

US-08-026-138E-10

Query Match 99.4%; Score 540; DB 1; Length 920;
Best Local Similarity 99.1%; Pred. No. 3.4e-57;
Matches 110; Conservative 1; Mismatches 0; Indels

QY	1	IILLVSDDHGEGRAAQKRLFTLLERESKAEKVLFQDPGKNTVTALLMEARELEEARVILS	60
Db	145	IILLVSDDHGEGRAAQKRLFTLLERESKAEKVLFQDPGKNTVTALLMEARELEEARVILS	204
QY	61	ASEDDAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGGIIGLOLIN	111
Db	205	ASEDDAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGGIIGLOLIN	255

RESULT 3
US-08-231-193A-14
: Sequence 14. Application US/08231193A

Patent No. 5849895
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: U.S.A.
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION: 536

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, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/052,459
, FILING DATE: 20-APR-1993
, CLASSIFICATION: 536
, ATTORNEY/AGENT INFORMATION:
, NAME: Seidman, Stephanie
, REGISTRATION NUMBER: 33,779
, REFERENCE/DOCKET NUMBER: 6362-9383
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 619-238-0999
, TELEFAX: 619-238-0062
, INFORMATION FOR SEQ ID NO: 14:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 922 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
, US-08-231-193A-14

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Query Match 99.1%; Score 538; DB 2; Length 922;
Best Local Similarity 98.2%; Pred. No. 5.9e-57;
Matches 109; Conservative 2; Mismatches 0; Indels

[illegible]

Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 4

US-08-231-193A-20
; Sequence 20, Application US/08231193A
; Patent No. 5849895

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.

APPLICANT: Lu, Chin-Chun

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR

TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: U.S.A.

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/231,193A

FILING DATE: 20-APR-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/052,459

FILING DATE: 20-APR-1993

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 922 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-231-193A-20

Query Match

Best Local Similarity 99.1%; Score 538; DB 2; Length 922;

Mismatches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILLVSDHGGRAAKRLETLLEERESKAQKVLQFDGPKNTVALLMEARELEAVIILS 60

Db 163 ILLVSDHGGRAAKRLETLLEERESKAQKVLQFDGPKNTVALLMEARELEAVIILS 222

Qy 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111

Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 5

US-08-486-273A-14
; Sequence 14, Application US/08486273A
; Patent No. 5985586

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie P.

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen W.

APPLICANT: Lu, Chin-Chun

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA

TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: U.S.A.

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,273A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/231,193

FILING DATE: 20-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383B

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 922 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-486-273A-14

Query Match

Best Local Similarity 99.1%; Score 538; DB 2; Length 922;

Mismatches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILLVSDHGGRAAKRLETLLEERESKAQKVLQFDGPKNTVALLMEARELEAVIILS 60

Db 163 ILLVSDHGGRAAKRLETLLEERESKAQKVLQFDGPKNTVALLMEARELEAVIILS 222

Qy 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111

Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 6

US-08-486-273A-20

; Sequence 20, Application US/08486273A

; Patent No. 5985586

; GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie P.

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen W.

APPLICANT: Lu, Chin-Chun

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA

TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: U.S.A.

ZIP: 92101-2926

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

RESULT 7
US-08-480-474-14
: Sequence 14, Application US/08480474
: Patent No. 6033865
: GENERAL INFORMATION:
: APPLICANT: Daggett, Lorrie P.
: APPLICANT: Ellis, Steven B.
: APPLICANT: Liaw, Chen W.
: APPLICANT: Lu, Chin-Chun
: TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
: TITLE OF INVENTION: SAME AND USES THEREFOR
: NUMBER OF SEQUENCES: 54
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: CA
: COUNTRY: U.S.A.
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/480,474
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 6362-9382B
: TELECOMMUNICATION INFORMATION:

0v 1 IILLVSDPDHEGRAAKRLETLLEERESKAEKVLOFDPGTKNVNTALLMEARELEARVILS 60

Db 163 IILLVSDDEGAAKRLTLEERESKAEKVLQDPGKNTVNTALLMEARELEAVIILS 222
QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111
Db 223 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

RESULT 9
US-08-940-086A-14
; Sequence 14, Application US/08940086A
; Patent No. 6111091
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940.086A
; FILING DATE: 29-SEPT-97
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,449
; FILING DATE: 20-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9383C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 450-8499
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 922 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-940-086A-14

Query Match 99.1%; Score 538; DB 3; Length 922;
Best Local Similarity 98.2%; Pred. No. 5.9e-57;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDDEGAAKRLTLEERESKAEKVLQDPGKNTVNTALLMEARELEAVIILS 60
Db 163 IILLVSDDEGAAKRLTLEERESKAEKVLQDPGKNTVNTALLMEARELEAVIILS 222
QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111
Db 223 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

RESULT 10
US-08-940-086A-20

; Sequence 20, Application US/08940086A
; Patent No. 6111091
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940.086A
; FILING DATE: 29-SEPT-97
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,449
; FILING DATE: 20-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9383C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 450-8499
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 922 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-940-086A-20

Query Match 99.1%; Score 538; DB 3; Length 922;
Best Local Similarity 98.2%; Pred. No. 5.9e-57;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDDEGAAKRLTLEERESKAEKVLQDPGKNTVNTALLMEARELEAVIILS 60
Db 163 IILLVSDDEGAAKRLTLEERESKAEKVLQDPGKNTVNTALLMEARELEAVIILS 222
QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111
Db 223 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

RESULT 11

US-08-231-193A-2
; Sequence 2, Application US/08231193A
; Patent No. 5849895
; GENERAL INFORMATION:

; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; NUMBER OF SEQUENCES: 63

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 938 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-193A-2

Query Match 99.1%; Score 538; DB 2; Length 938;
Best Local Similarity 98.2%; Pred. No. 6.1e-57;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILLVSDHDEGRAAKRLTLLERESKAELVQDPGKNTALLMEARELEAVIILS 60
Db 163 ILLVSDHDEGRAAKRLTLLERESKAELVQDPGKNTALLMEARELEAVIILS 222
Q 61 ASEDAAATVYRAAAMLNMTGSGYVWLGVGERISGNALRYAPDGIIGLQLIN 111
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLGVGERISGNALRYAPDGIIGLQLIN 273

RESULT 12
US-08-486-273A-2
; Sequence 2, Application US/08486273A
; Patent No. 5985586
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,273A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 938 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-273A-2

Query Match 99.1%; Score 538; DB 2; Length 938;
Best Local Similarity 98.2%; Pred. No. 6.1e-57;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ILLVSDHDEGRAAKRLTLLERESKAELVQDPGKNTALLMEARELEAVIILS 60
Db 163 ILLVSDHDEGRAAKRLTLLERESKAELVQDPGKNTALLMEARELEAVIILS 222
Q 61 ASEDAAATVYRAAAMLNMTGSGYVWLGVGERISGNALRYAPDGIIGLQLIN 111
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLGVGERISGNALRYAPDGIIGLQLIN 273

RESULT 13
US-08-480-474-2
; Sequence 2, Application US/08480474
; Patent No. 6033865
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
; TITLE OF INVENTION: SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,474
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9382B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0062
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 2:
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Query Match 99.1%; Score 538; DB 3; Length 938;
Best Local Similarity 98.2%; Pred. No. 6.1e-57;

US-08-940-086A-2

277 WGET TC7.00 EN

D6 223 ASEDDAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGILGLQLIN 2/3

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: November 1, 2001, 16:24:05 ; Search time 21.33 Seconds
(without alignments)
315.483 Million cell updates/sec

Title: US-09-652-345-6
Perfect score: 543
Sequence: 1 IILLVSDDEHRAAQRRLT.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Minimum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	100.0	111	22 AAB74434	Human NMDA recepto
2	540	99.4	920	15 AAR49043	NMDA receptor chan
3	540	99.4	920	15 AAR49044	NMDA receptor chan
4	538	99.1	885	15 AAR57328	NMDAR1-1. Homo sa
5	538	99.1	885	16 AAR80973	Human excitatory a
6	538	99.1	918	15 AAR66042	Human N-methyl-D-a
7	538	99.1	922	15 AAR66046	Human NMDA recepto
8	538	99.1	922	15 AAR66043	Human N-methyl-D-a
9	538	99.1	922	20 AAR85580	Human N-methyl-D-a
10	538	99.1	922	20 AAR85577	Human N-methyl-D-a
11	538	99.1	922	21 AAB26216	Human N-methyl-D-a

12	538	99.1	922	21	AAB26219	Human N-methyl-D-a
13	538	99.1	922	21	AAV56114	Human N-methyl-D-a
14	538	99.1	922	21	AAV56117	Human N-methyl-D-a
15	538	99.1	938	15	AAR66035	Human N-methyl-D-a
16	538	99.1	938	15	AAW85572	Human N-methyl-D-a
17	538	99.1	938	21	AAB26211	Human N-methyl-D-a
18	538	99.1	938	21	AAV56109	Human N-methyl-D-a
19	538	99.1	976	15	AAR66047	Human NMDA recepto
20	538	99.1	976	20	AAW85581	Human N-methyl-D-a
21	538	99.1	976	20	AAB26220	Human N-methyl-D-a
22	538	99.1	976	21	AAV56118	Human N-methyl-D-a
23	532	98.0	885	15	AAW55530	Human NMDA Rle rec
24	532	98.0	922	15	AAW55531	Human NMDA Rle rec
25	532	98.0	938	15	AAW55532	Human NMDA Rle rec
26	517.5	95.3	943	15	AAR66054	Human N-methyl-D-a
27	517.5	95.3	943	20	AAW85588	Human N-methyl-D-a
28	517.5	95.3	943	21	AAB26227	Human NMDAR1-163-d
29	517.5	95.3	943	21	AAV56123	Human NMDA recepto
30	517.5	95.3	959	15	AAR66048	Human N-methyl-D-a
31	517.5	95.3	959	20	AAW85582	Human N-methyl-D-a
32	517.5	95.3	959	21	AAB26221	Human N-methyl-D-a
33	517.5	95.3	959	21	AAV56119	Human N-methyl-D-a
34	517.5	95.3	997	15	AAR66055	Human NMDA recepto
35	517.5	95.3	997	20	AAW85589	Human N-methyl-D-a
36	517.5	95.3	997	21	AAB26228	Human N-methyl-D-a
37	517.5	95.3	997	21	AAV56126	Human NMDAR1-163-d
38	513	94.5	111	22	AAB74435	Human NMDA recepto
39	400	73.7	854	15	AAR66052	Human N-methyl-D-a
40	400	73.7	854	20	AAW85586	Human N-methyl-D-a
41	400	73.7	854	21	AAB26225	Human N-methyl-D-a
42	400	73.7	854	21	AAV56123	Human NMDAR1-delta
43	400	73.7	870	15	AAR66051	Human NMDA recepto
44	400	73.7	870	20	AAW85585	Human N-methyl-D-a
45	400	73.7	870	21	AAB26224	Human N-methyl-D-a

ALIGNMENTS

RESULT 1	
AAB74434	ID AAB74434 standard; protein; 111 AA.
XX	AC AAB74434;
XX	DT 29-MAY-2001 (first entry)
XX	DE Human NMDA receptor NR1011 subunit.
XX	KW Human; NMDA receptor; CNS; N-methyl-D-aspartate receptor; modulator;
KW	neuropathic pain; drug dependency; epilepsy; glaucoma;
KW	neurodegenerative disease; amyotrophic lateral sclerosis; anxiety;
KW	brain cell death; ischaemia; stroke; trauma.
XX	OS Homo sapiens.
XX	PN WO200116601-A1.
XX	PD 08-MAR-2001.
XX	PF 31-AUG-2000; 2000WO-US23985.
XX	PR 31-AUG-1999; 99US-0151802.
XX	PA (UYBO-) UNIV BOSTON.
XX	PI Farb DH, Russek S, Jang M, Gibbs T;
XX	DR WPI; 2001-257712/26.
XX	PT Identifying a subunit specific modulator of the NMDA receptor for
PT	treating diseases such as neurodegenerative diseases, and ischemia
PT	comprises assaying for an increase or decrease in receptor activity in

PT the presence of the modulator -

XX *

PS Example 5; Fig 23; 135pp; English.

XX

CC The present invention describes a method of identifying subunit specific

CC modulators of the N-methyl-D-aspartate (NMDA) receptor, involving

CC contacting a number of different receptors with a neurotransmitter

CC recognition site in the presence of the agent of interest, and assaying

CC for receptor activity. Modulators of this type are useful in the

CC treatment of neuropathic pain, drug withdrawal and dependency, epilepsy,

CC glaucoma, chronic neurodegenerative diseases, amyotrophic lateral

CC sclerosis, anxiety disorders, brain cell death, ischaemia, stroke and

CC trauma.

XX

SQ Sequence 111 AA;

Query Match 100.0%; Score 543; DB 22; Length 111;

Best Local Similarity 100.0%; Pred. No. 2.9e-58;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHDEGRAQKRLTLLERESKAQKVLQFDGPKNTVNTALLMEARELEARVILS 60

Db 1 IILLVSDHDEGRAQKRLTLLERESKAQKVLQFDGPKNTVNTALLMEARELEARVILS 60

Qy 61 ASDDAATVYRAAAMNMTGSGYVWLGEREISGNALRYAPDGIIGLQLIN 111

Db 61 asddaatvyraaamlnmtgsgyvwlgereisgnalryapdgiiglqlin 111

RESULT 2

AAR49043

ID AAR49043 standard; Protein; 920 AA.

XX

AC AAR49043;

XX

DT 20-SEP-1994 (first entry)

XX

DE NMDA receptor channel subunit zeta-1-N598Q.

XX

KW NMDA; N-methyl-D-aspartate; receptor; channel; subunit;

KW brain; cerebellum; neurotransmission; synapse; memory;

KW learning; neurocyte; necrosis; cerebral ischemia;

KW status epilepticus; CNS; central nervous system.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Misc-difference 598 /note= "N598Q"

FT

XX

PN WO9404698-A.

XX

PD 03-MAR-1994.

XX

PF 12-AUG-1993; 93WO-JP01143.

XX

PR 12-AUG-1992; 92JP-0215017.

XX

PA (MITU) MITSUBISHI KASEI CORP.

XX

PI Mishina M;

XX

DR WPI; 1994-083212/10.

DR N-PSDB; AAQ55980.

XX

XX NMDA receptor channel epsilon and zeta sub-unit proteins -

PT obtained by Xenopus oocyte expression of modified receptor mRNA

XX

PS Claim 1; Page 21-27; 44pp; Japanese.

XX

XX NMDA receptor cDNA from a mouse cerebellum-derived library

CC is subjected to site-specific mutagenesis to give cDNA coding

CC

CC for the desired modified proteins. mRNA derived from this

CC is then expressed in Xenopus laevis oocytes.

CC The modified NMDA receptor channel subunit proteins (AAQ55979-81)

CC are useful as tools for investigation of the mechanism of

CC neurotransmission across synapses, the development of synapse

CC plasticity (basic to memory and learning), the development of

CC neurocyte necrosis as a result of disorders such as cerebral

CC ischemia and status epilepticus. This is necessary for understanding

CC the mechanisms of neurotransmission in the CNS and the organisation

CC and pathology of the brain, and in the development of drugs and

CC therapy for brain diseases and genetically determined disorders.

XX

SQ Sequence 920 AA;

Query Match 99.4%; Score 540; DB 15; Length 920;

Best Local Similarity 99.1%; Pred. No. 1.4e-56;

Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHDEGRAQKRLTLLERESKAQKVLQFDGPKNTVNTALLMEARELEARVILS 60

Db 145 IILLVSDHDEGRAQKRLTLLERESKAQKVLQFDGPKNTVNTALLMEARELEARVILS 204

Qy 61 ASDDAATVYRAAAMNMTGSGYVWLGEREISGNALRYAPDGIIGLQLIN 111

Db 205 asddaatvyraaamlnmtgsgyvwlgereisgnalryapdgiiglqlin 255

RESULT 3

AAR49044

ID AAR49044 standard; Protein; 920 AA.

XX

AC AAR49044;

XX

DT 20-SEP-1994 (first entry)

XX

DE NMDA receptor channel subunit zeta-1-ZAZ.

XX

KW NMDA; N-methyl-D-aspartate; receptor; channel; subunit;

KW brain; cerebellum; neurotransmission; synapse; memory;

KW learning; neurocyte; necrosis; cerebral ischemia;

KW status epilepticus; CNS; central nervous system.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Misc-difference 576..581 /note= "mouse-derived sequence altered

FT to TSDQSN"

FT

XX

PN WO9404698-A.

XX

PD 03-MAR-1994.

XX

PF 12-AUG-1993; 93WO-JP01143.

XX

PR 12-AUG-1992; 92JP-0215017.

XX

PA (MITU) MITSUBISHI KASEI CORP.

XX

PI Mishina M;

XX

DR WPI; 1994-083212/10.

DR N-PSDB; AAQ55981.

XX

XX NMDA receptor channel epsilon and zeta sub-unit proteins -

PT obtained by Xenopus oocyte expression of modified receptor mRNA

XX

PS Claim 1; Page 27-33; 44pp; Japanese.

XX

XX NMDA receptor cDNA from a mouse cerebellum-derived library

CC is subjected to site-specific mutagenesis to give cDNA coding

CC for the desired modified proteins. mRNA derived from this

CC

100

PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 XX
 PI Adams S, Fantaskie R, Foldes R, Kamboj R;
 XX
 DR N-PSDB; AAQ999964.
 XX
 DR WPI; 1995-329869/43.
 XX
 DR N-PSDB; AAQ999964.
 XX
 PT New modulatory proteins of human CNS receptors - used to develop
 PT prods. for use in identifying agents for the treatment of
 PT neurological disease conditions
 XX
 XX Disclosure; Fig.8; 99pp; English.
 XX
 CC This NMDA1-1 excitatory amino acid (EAA) receptor binds NMDA
 CC (N-methyl-D-aspartate) as well as glutamate. It may be used to
 CC construct a human heteromeric receptor complex which consists of
 CC this NMDA1-1 receptor and a modulatory protein such as NR2A-1,
 CC NR3-1 and NR4-1. This complex has electrophysiological properties
 CC which are distinct from those of a homodimeric receptor complex
 CC formed from the NMDA1-1 receptor alone. Transformed cells which
 CC heteromerically produce a modulatory protein and this NMDA1-1
 CC receptor may be used for screening candidate ligands for
 CC interaction with the heteromeric receptor. Any ligands that are
 CC identified can be used as agonists or antagonists in the treatment
 CC of neurological disease.
 XX
 SQ Sequence 885 AA;

Query Match 99.1%; Score 538; DB 16; Length 885;
 Best Local Similarity 98.2%; Pred. No. 2.3e-56;
 Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IILLVSDHDEGRAAQKRLTLLERESKAEKVLPDGTGKNTALLMEARELEARVILS 60
 Db 163 IILLVSDHDEGRAAQKRLTLLERESKAEKVLPDGTGKNTALLMEARELEARVILS 222
 QY 61 ASDDAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
 Db 223 asddaatyraaaminmtgsgyvwlvgereisgnalryapdgiilqlin 273

RESULT 6
 AAR66042
 ID AAR66042 standard; Protein; 918 AA.
 XX AAR66042;
 XX
 DT 03-JUL-1995 (first entry)
 XX
 DE Human N-methyl-D-aspartate receptor subunit 1A a.a. seq. in clone NMDA10.
 XX
 KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
 KW glutamate; hippocampus; rat; pcdNAL; NMDA receptor; antagonist.
 XX
 OS Homo sapiens.
 XX
 PN WO9424284-A.
 XX
 PD 27-OCT-1994.
 XX
 PF 20-APR-1994; 94WO-US04387.
 XX
 PR 20-APR-1993; 93US-0052449.
 XX
 PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX
 PI Daggett LP, Ellis SB, Liaw CW, Lu C;
 XX
 DR WPI; 1994-341863/42.
 DR N-PSDB; AAQ79384.
 XX
 PT Isolated DNA encoding a human N-methyl-D-aspartate receptor

PT subunit - used as probes in the identification and isolation of
 PT nucleic acids encoding related receptor subunits.
 XX
 PS Claim 5; Page 91-95; 156pp; English.
 XX
 CC The amino acid sequence of the novel N-methyl-D-aspartate (NMDA)
 CC receptor 1A (NMDA1A) from clone NMDA10 (sequence not given in the
 CC specification). This clone was one of 8 isolated from a cDNA library
 CC derived from human hippocampal tissue RNA using probes corresponding to
 CC sequences in the rat NMDA1A receptor cDNA. The 2.1 kb EcoRI-HindIII
 CC fragment from clone NMDA11 (AAQ79385) containing the 5' portion of the
 CC gene, with the 3.3 kb BglII-EcoRI fragment of clone NMDA10, containing
 CC the 3' portion of the gene, were ligated to generate the full length
 CC sequence (AAQ79370) of the NMDA1A gene in plasmid pCDNAL1. The resultant
 CC clone, NMDA1A, contains 261 bp of 5' untranslated DNA, the entire coding
 CC region for the NMDA1A receptor and 1220 bp of 3' untranslated DNA. The
 CC NMDA10 clone covers bases 320-3402 of the full length sequence. The NMDA
 CC receptor contains a second subunit selected from the subunits 2A
 CC (AAQ79375), 2B (AAQ79377), 2C (AAQ79372) and 2D (AAQ79378). The receptor
 CC forms part of a family of NMDA receptors which have cation-selective
 CC channels and bind glutamate and NMDA. Based on the sequences of clones:
 CC NMDA10, NMDA11, NMDA7 (AAQ79386) and NMDA3 (AAQ79387), a series of
 CC variants (AAQ79388-98) of the NMDA1A receptor gene were constructed.
 CC The expression of the genes allows the reconstruction of the NMDA
 CC receptor. The complete receptor can be used to identify compounds which
 CC bind or are antagonistic to the human NMDA receptor.
 XX
 SQ Sequence 918 AA;

Query Match 99.1%; Score 538; DB 15; Length 918;
 Best Local Similarity 98.2%; Pred. No. 2.5e-56;
 Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IILLVSDHDEGRAAQKRLTLLERESKAEKVLPDGTGKNTALLMEARELEARVILS 60
 Db 143 IILLVSDHDEGRAAQKRLTLLERESKAEKVLPDGTGKNTALLMEARELEARVILS 202
 QY 61 ASDDAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
 Db 203 asddaatyraaaminmtgsgyvwlvgereisgnalryapdgiilqlin 253

RESULT 7
 AAR66046
 ID AAR66046 standard; Protein; 922 AA.
 XX AAR66046;
 XX
 DT 04-JUL-1995 (first entry)
 XX
 DE Human NMDA receptor subunit NMDA1-delta363 protein.
 XX
 KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
 KW glutamate; hippocampus; rat; pcdNAL; NMDA receptor; antagonist.
 XX
 OS Homo sapiens.
 XX
 PN WO9424284-A.
 XX
 PD 27-OCT-1994.
 XX
 PF 20-APR-1994; 94WO-US04387.
 XX
 PR 20-APR-1993; 93US-0052449.
 XX
 PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX
 XX

PI Daggett LP, Ellis SB, Liaw CW, Lu C;
XX WPI: 1994-341863/42.
DR N-PSDB; AAQ79388.
XX
XX Isolated DNA encoding a human N-methyl-D-aspartate receptor
PT subunit - used as probes in the identification and isolation of
PT nucleic acids encoding related receptor subunits.
XX
XX
PS Claim 5; Page 91-95; 156pp; English.
XX
CC The amino acid sequence of the novel N-methyl-D-aspartate (NMDA)
CC receptor 1A (NMDAR1A) clone NMDAR1-delta363 (sequence not given in the
CC specification). The clone contains a deletion of 121 a.a. between
CC a.a. 900-938 of the NMDAR1A sequence (AAQ79370). The clone uses an
CC alternative stop codon at bases 3391-3 of the NMDAR1A sequence. This
CC produces an alternative 22 a.a. at the C-terminus of this clone. This
CC variant clone was constructed, by recombination, using the clones:
CC NMDA10 (AAQ79384), NMDA11 (AAQ79385), NMDA7 (AAQ79386) and NMDA3
CC (AAQ79387). These clones were used to construct a series of variants
CC (AAQ79388-98) of the NMDAR1A receptor gene. The NMDAR1A gene isolated
CC from a cDNA library derived from human hippocampal tissue RNA using
CC probes corresponding to sequences in the rat NMDAR1A receptor DNA. The
CC 2.1 kb EcoRI-HindIII fragment from clone NMDA11, containing the 5',
CC portion of the gene, with the 3.3 kb BglII-EcoRI fragment of clone
CC NMDA10, containing the 3' portion of the gene, were ligated to generate
CC the full length sequence (AAQ79370) of the NMDAR1A gene in plasmid
CC pCDNA1. The resultant clone, NMDAR1A, contains tcc 261 bp of 5',
CC untranslated DNA, the entire coding region for the NMDAR1A receptor and
CC 1220 bp of 3' untranslated DNA. The NMDA receptor contains a second
CC subunit selected from the subunits 2A (AAQ79375), 2B (AAQ79377), 2C
CC (AAQ79372) and 2D (AAQ79378). The receptor forms part of a family of NMDA
CC receptors which have cation-selective channels and bind glutamate and
CC NMDA. The expression of the genes allows the reconstruction of the NMDA
CC receptor. The complete receptor can be used to identify compounds which
CC bind or are antagonistic to the human NMDA receptor.
XX
XX Sequence 922 AA;
SQ

Query Match 99.1%; Score 538; DB 15; Length 922;
Best Local Similarity 98.2%; Pred. No. 2.5e-56;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLTLLERESKAELVQFDPTGKNTVNTALLMEARELEAVIILS 60
Db 163 IILLVSDHDEGRAAKRLTLLERESKAELVQFDPTGKNTVNTALLMEARELEAVIILS 222

QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
Db 223 aseddaatvyr aaamlnmtgsgyvwlvger eisgnalry apdgiilgqlin 273

RESULT 8
AA66043
ID AAR66043 standard; Protein; 922 AA.
AC AAR66043;
XX
XX 03-JUL-1995 (first entry)
XX
XX Human N-methyl-D-aspartate receptor subunit 1A a.a. seq. clone NMDA11.
XX N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
KW glutamate; hippocampus; rat; pCDNA1; NMDA receptor; antagonist.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 900..901
FT /note= "38 a.a. deletion of the C-terminal NMDAR1A a.a.
FT sequence between these residues"
XX

PN WO9424284-A.
XX
PD 27-OCT-1994.
XX
PF 20-APR-1994; 94WO-US04387.
XX
PR 20-APR-1993; 93US-0052449.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Daggett LP, Ellis SB, Liaw CW, Lu C;
XX
XX WPI: 1994-341863/42.
DR N-PSDB; AAQ79385.
XX
XX Isolated DNA encoding a human N-methyl-D-aspartate receptor
PT subunit - used as probes in the identification and isolation of
PT nucleic acids encoding related receptor subunits.
XX
XX
PS Claim 5; Page 91-95; 156pp; English.
XX
CC The amino acid sequence of the novel N-methyl-D-aspartate (NMDA)
CC receptor 1A (NMDAR1A) from clone NMDA11 (sequence not given in the
CC specification). The clone contains a deletion of the residues 901-938 of
CC the NMDAR1A sequence (AAR66035). The clone uses the next in-frame stop
CC codon at pos. 3391-3 of the NMDAR1A DNA sequence (AAQ79370). This
CC encodes an alternative 22 a.a. at the C-terminus of the protein. This
CC clone was one of 8 isolated from a cDNA library derived from human
CC hippocampal tissue RNA using probes corresponding to sequences in the rat
CC NMDAR1A receptor DNA. The 2.1 kb EcoRI-HindIII fragment from clone NMDA11
CC containing the 5' portion of the gene, with the 3.3 kb BglII-EcoRI
CC fragment of clone NMDA10 (AAQ79384), containing the 3' portion of the
CC gene, were ligated to generate the full length sequence (AAQ79370) of the
CC NMDAR1A gene in plasmid pCDNA1. The entire coding region for the NMDAR1A
CC receptor and 1220 bp of 3' untranslated DNA. The NMDA receptor contains
CC a second subunit selected from the subunits 2A (AAQ79375), 2B (AAQ79377),
CC 2C (AAQ79372) and 2D (AAQ79378). The receptor forms part of a family of
CC NMDA receptors which have cation-selective channels and bind glutamate
CC and NMDA. Based on the sequences of clones: NMDA10, NMDA11, NMDA7
CC (AAQ79386) and NMDA3 (AAQ79387), a series of variants (AAQ79388-98) of
CC the NMDAR1A receptor gene were constructed. The expression of the genes
CC allows the reconstruction of the NMDA receptor. The complete receptor
CC can be used to identify compounds which bind or are antagonistic to the
CC human NMDA receptor.
XX
XX Sequence 922 AA;
SQ

Query Match 99.1%; Score 538; DB 15; Length 922;
Best Local Similarity 98.2%; Pred. No. 2.5e-56;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLTLLERESKAELVQFDPTGKNTVNTALLMEARELEAVIILS 60
Db 163 IILLVSDHDEGRAAKRLTLLERESKAELVQFDPTGKNTVNTALLMEARELEAVIILS 222

QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
Db 223 aseddaatvyr aaamlnmtgsgyvwlvger eisgnalry apdgiilgqlin 273

RESULT 9
AAW85580
ID AAW85580 standard; Protein; 922 AA.
XX
XX AAW85580;
AC
XX
XX 23-FEB-1999 (first entry)
XX
XX Human N-methyl-D-aspartate receptor subunit NMDAR1-delta363.
XX Human; N-methyl-D-aspartate receptor; NMDAR1;
KW

KW NMDA-activated cation-selective ion channel; glutamate receptor.

XX Homo sapiens.

XX US5849895-A.

XX 15-DEC-1998.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1993; 93US-0052449.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Daggett LP, Lu C;

XX WPI; 1999-069812/06.

XX N-PSDB; AAV82897.

PT DNA encoding N-methyl-D-aspartate receptor subunit - useful for the assembly of functional glutamate receptor subunits

PS Disclosure; Columns 123-128; 203pp; English.

XX The present sequence represents a human N-methyl-D-aspartate (NMDA) receptor (NMDAR) subunit, designated NMDAR1-delta363. The nucleic acid sequence does not contain the 363 nucleotides 2962-3324, as set forth in AAV82887. The NMDAR subunits contribute to the formation of NMDA-activated cation-selective ion channels. In addition to being useful for the production of NMDA receptor subunit proteins, the nucleic acids are also useful as probes to identify and isolate nucleic acids encoding related receptor subunits. Functional glutamate receptors can be assembled from several NMDA receptor subunit proteins of one type (homomeric) or from combinations of subunit proteins of different types (heteromeric). The present invention also comprises methods for using such receptor subunits to identify and characterize compounds which affect the function of such receptors, e.g. agonists, antagonists and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown protein(s) are functional as NMDA receptor subunits.

XX Sequence 922 AA;

Query Match 99.1%; Score 538; DB 20; Length 922;
Best Local Similarity 98.2%; Pred. No. 2.5e-56;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILLVSDHDEGRAAKRLTLLERESKAERVLQDPGKNTVALLMEARELEARVILS 60
|||||
Db 163 ILLVSDHDEGRAAKRLTLLERESKAERVLQDPGKNTVALLMEARELEARVILS 222
|||||

QY 61 ASDDAATVYRAAAMLNMTGSGYVWLVGREISGNALRYAPDGIIGLQLIN 111
|||||
Db 223 ASDDAATVYRAAAMLNMTGSGYVWLVGREISGNALRYAPDGIIGLQLIN 273
|||||

RESULT 10

ID AAW85577 standard; Protein; 922 AA.

XX AAW85577;

XX 23-FEB-1999 (first entry)

XX Human N-methyl-D-aspartate receptor subunit.

XX Human; N-methyl-D-aspartate receptor; NMDAR1;

XX NMDA-activated cation-selective ion channel; glutamate receptor.

XX Homo sapiens.

XX

PN US5849895-A.

PD 15-DEC-1998.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1993; 93US-0052449.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Daggett LP, Lu C;

XX WPI; 1999-069812/06.

XX N-PSDB; AAV82894.

PT DNA encoding N-methyl-D-aspartate receptor subunit - useful for the assembly of functional glutamate receptor subunits

PS Example 1; Columns 97-104; 203pp; English.

XX The present sequence represents a human N-methyl-D-aspartate (NMDA) receptor subunit (NMDAR1). The nucleic acid sequence does not contain the 363 nucleotides 2962-3324 or the 781 terminal 3' nucleotides, as set forth in AAV82887. The cDNA sequence is derived from clone CCDA11. The NMDAR subunits contribute to the formation of NMDA-activated cation-selective ion channels. In addition to being useful for the production of NMDA receptor subunit proteins, the nucleic acids are also useful as probes to identify and isolate nucleic acids encoding related receptor subunits. Functional glutamate receptors can be assembled from several NMDA receptor subunit proteins of one type (homomeric) or from combinations of subunit proteins of different types (heteromeric). The present invention also comprises methods for using such receptor subunits to identify and characterize compounds which affect the function of such receptors, e.g. agonists, antagonists and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown protein(s) are functional as NMDA receptor subunits.

XX Sequence 922 AA;

Query Match 99.1%; Score 538; DB 20; Length 922;
Best Local Similarity 98.2%; Pred. No. 2.5e-56;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILLVSDHDEGRAAKRLTLLERESKAERVLQDPGKNTVALLMEARELEARVILS 60
|||||
Db 163 ILLVSDHDEGRAAKRLTLLERESKAERVLQDPGKNTVALLMEARELEARVILS 222
|||||

QY 61 ASDDAATVYRAAAMLNMTGSGYVWLVGREISGNALRYAPDGIIGLQLIN 111
|||||
Db 223 ASDDAATVYRAAAMLNMTGSGYVWLVGREISGNALRYAPDGIIGLQLIN 273
|||||

RESULT 11

ID AAB26216 standard; Protein; 922 AA.

XX AAB26216;

XX 23-FEB-2001 (first entry)

XX Human N-methyl-D-aspartate receptor subunit NMDAR1A #2.

XX Human; N-methyl-D-aspartate receptor; NMDA; NMDAR1A; ionotropic;

XX glutamate receptor; drug screening; animal model; disease diagnosis;

XX genetic screening.

XX Homo sapiens.

XX US6111091-A.

XX

PD 29-AUG-2000.
 XX
 PF 29-SEP-1997; 97US-0940086.
 XX
 PR 20-APR-1994; 94US-0231193.
 PR 20-APR-1993; 93US-0052449.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Daggett LP, Lu C;
 XX
 DR WPI; 2000-578607/54.
 DR N-PSDB; AAA95017.
 XX
 PT Novel DNA fragment encoding human N-methyl-D-aspartate receptor subunit
 PT for identifying mutations and for developing drugs against various
 PT disease states -
 XX
 PS Disclosure; column 99-104; 205pp; English.
 XX
 CC The present sequence is a subunit (designated NMDAR1A) of the human
 CC N-methyl-D-aspartate (NMDA) receptor. This is an ionotropic glutamate
 CC receptor which contains cation-specific ligand-gated ion channels. The
 CC protein and its coding sequence can be used in disease diagnosis and in
 CC research to identify other, similar proteins. They can also be used as
 CC probes, for example in genetic screening, and in drug screening, as well
 CC as enabling the production of animal disease models.
 XX
 SQ Sequence 922 AA;
 XX
 Query Match 99.1%; Score 538; DB 21; Length 922;
 Best Local Similarity 98.2%; Pred. No. 2.5e-56;
 Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IILLVSDHGEGRRAAKRLETLLERESKAQKVLQFDGPKNTVNTALLMEARELEAVIILS 60
 DB 163 IILLVSDHGEGRRAAKRLETLLERESKAQKVLQFDGPKNTVNTALLMEARELEAVIILS 222
 QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111
 DB 223 asddaatvyraaamlnmtsgsyvwlvgereisgnalryapdgiilgqlin 273
 XX
 RESULT 12
 AAB26219
 ID AAB26219 standard; Protein; 922 AA.
 XX
 AC AAB26219;
 XX
 DT 23-FEB-2001 (first entry)
 DE Human N-methyl-D-aspartate receptor subunit NMDAR1A #5.
 XX
 KW Human; N-methyl-D-aspartate receptor; NMDA; NMDAR1A; ionotropic;
 KW glutamate receptor; drug screening; animal model; disease diagnosis;
 KW genetic screening.
 XX
 OS Homo sapiens.
 XX
 PN US6111091-A.
 XX
 PD 29-AUG-2000.
 XX
 PF 29-SEP-1997; 97US-0940086.
 XX
 PR 20-APR-1994; 94US-0231193.
 PR 20-APR-1993; 93US-0052449.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Daggett LP, Lu C;
 XX

DR WPI; 2000-578607/54.
 DR N-PSDB; AAA95020.
 XX
 PT Novel DNA fragment encoding human N-methyl-D-aspartate receptor subunit
 PT for identifying mutations and for developing drugs against various
 PT disease states -
 XX
 PS Disclosure; column 123-128; 205pp; English.
 XX
 CC The present sequence is a subunit (designated NMDAR1A) of the human
 CC N-methyl-D-aspartate (NMDA) receptor. This is an ionotropic glutamate
 CC receptor which contains cation-specific ligand-gated ion channels. The
 CC protein and its coding sequence can be used in disease diagnosis and in
 CC research to identify other, similar proteins. They can also be used as
 CC probes, for example in genetic screening, and in drug screening, as well
 CC as enabling the production of animal disease models.
 XX
 SQ Sequence 922 AA;
 XX
 Query Match 99.1%; Score 538; DB 21; Length 922;
 Best Local Similarity 98.2%; Pred. No. 2.5e-56;
 Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IILLVSDHGEGRRAAKRLETLLERESKAQKVLQFDGPKNTVNTALLMEARELEAVIILS 60
 DB 163 IILLVSDHGEGRRAAKRLETLLERESKAQKVLQFDGPKNTVNTALLMEARELEAVIILS 222
 QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111
 DB 223 asddaatvyraaamlnmtsgsyvwlvgereisgnalryapdgiilgqlin 273
 XX
 RESULT 13
 AAY56114
 ID AAY56114 standard; Protein; 922 AA.
 XX
 AC AAY56114;
 XX
 DT 08-FEB-2000 (first entry)
 DE Human N-methyl-D-aspartate receptor 1 subunit SEQ ID NO:14.
 XX
 KW Human; N-methyl-D-aspartic acid; N-methyl-D-aspartic acid receptor;
 KW NMDA; NMDAR; receptor subunit; cation-selective channel; modulator;
 KW glutamate binding; glutamate receptor; NMDA receptor subunit;
 KW neuronal process; fast excitatory synaptic transmission; regulation;
 KW neurotransmitter release; long-term potentiation; learning; memory;
 KW developmental synaptic plasticity; hypoxic-ischaemic damage;
 KW neuronal cell death; epileptiform seizure; neurodegenerative disorder.
 XX
 OS Homo sapiens.
 XX
 PN US5985586-A.
 XX
 PD 16-NOV-1999.
 XX
 PF 06-JUN-1995; 95US-0486273.
 XX
 PR 20-APR-1994; 94US-0231193.
 PR 20-APR-1993; 93US-0052449.
 XX
 PA (SIBI-) SIBIA NEUROSCIENCES INC.
 XX
 PI Daggett LP, Ellis SB, Lu C, Liaw CW;
 XX
 DR WPI; 2000-022277/02.
 DR N-PSDB; AAZ38708.
 XX
 PT Identifying modulators of human N-methyl-D-aspartate receptors -
 XX Claim 4; Column 97-104; 202pp; English.
 PS

CC A method has been developed for identifying modulators of human
 CC N-methyl-D-aspartate (NMDA) receptors. The method may be used for
 CC identifying modulators of human NMDA receptors. The modulators may
 CC be useful in controlling a wide range of neuronal processes including
 CC fast excitatory synaptic transmission, regulation of neurotransmitter
 CC releases, long-term potentiation, learning and memory, developmental
 CC synaptic plasticity, hypoxic-ischaemic damage and neuronal cell death,
 CC epileptiform seizures and the pathology of several neurodegenerative
 CC disorders. AA238701 to AA238736, and AA56109 to AA56135 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 922 AA;

Query Match 99.1%; Score 538; DB 21; Length 922;

Best Local Similarity 98.2%; Pred. No. 2.5e-56;

Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHGEGRRAAOKRLETLLEERESKAELVQDPGCTKNVTALLMEARELEARVILS 60
 |||||
 Db 163 IILLVSDHGEGRRAAOKRLETLLEERESKAELVQDPGCTKNVTALLMEARELEARVILS 222

Qy 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111

Db 223 asddaatvyr aamnm tsg yv wlv g e r e i s g n a l r y a p d g i i g l q l i n 273

RESULT 14

AA56117

AA56117 standard; Protein; 922 AA.

XX AC AA56117;

XX 08-FEB-2000 (first entry)

XX Human N-methyl-D-aspartate receptor 1 subunit SEQ ID NO:20.

XX Human; N-methyl-D-aspartic acid; N-methyl-D-aspartic acid receptor;
 KW NMDA; NMDAR; receptor subunit; cation-selective channel; modulator;
 KW glutamate binding; glutamate receptor; NMDA receptor subunit;
 KW neuronal processes; fast excitatory synaptic transmission; regulation;
 KW neurotransmitter release; long-term potentiation; learning; memory;
 KW developmental synaptic plasticity; hypoxic-ischaemic damage;
 KW neuronal cell death; epileptiform seizure; neurodegenerative disorder.

XX Homo sapiens.

XX US5985586-A.

XX 16-NOV-1999.

XX 06-JUN-1995; 95US-0486273.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1993; 93US-0052449.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Daggett LP, Ellis SB, Liaw CW;

XX WPI; 2000-022277/02.

XX N-PSDB; AA238711.

XX Identifying modulators of human N-methyl-D-aspartate receptors -

XX Claim 4; Column 123-128; 202pp; English.

XX A method has been developed for identifying modulators of human
 CC N-methyl-D-aspartate (NMDA) receptors. The method may be used for
 CC identifying modulators of human NMDA receptors. The modulators may
 CC be useful in controlling a wide range of neuronal processes including
 CC fast excitatory synaptic transmission, regulation of neurotransmitter
 CC releases, long-term potentiation, learning and memory, developmental

CC synaptic plasticity, hypoxic-ischaemic damage and neuronal cell death,
 CC epileptiform seizures and the pathology of several neurodegenerative
 CC disorders. AA238701 to AA238736, and AA56109 to AA56135 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 922 AA;

Query Match 99.1%; Score 538; DB 21; Length 922;

Best Local Similarity 98.2%; Pred. No. 2.5e-56;

Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHGEGRRAAOKRLETLLEERESKAELVQDPGCTKNVTALLMEARELEARVILS 60
 |||||
 Db 163 IILLVSDHGEGRRAAOKRLETLLEERESKAELVQDPGCTKNVTALLMEARELEARVILS 222

Qy 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111

Db 223 asddaatvyr aamnm tsg yv wlv g e r e i s g n a l r y a p d g i i g l q l i n 273

RESULT 15

AA66035

ID AAR66035 standard; Protein; 938 AA.

XX AC AAR66035;

XX 03-JUL-1995 (first entry)

XX Human N-methyl-D-aspartate receptor subunit 1A.

XX N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
 KW glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist.

XX Homo sapiens.

XX WO9424284-A.

XX 27-OCT-1994.

XX 20-APR-1994; 94WO-US04387.

XX 20-APR-1993; 93US-0052449.

XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

XX Daggett LP, Ellis SB, Liaw CW, Lu C;

XX WPI; 1994-341863/42.

XX N-PSDB; AAQ79370.

XX Isolated DNA encoding a human N-methyl-D-aspartate receptor
 subunit - used as probes in the identification and isolation of
 nucleic acids encoding related receptor subunits.

XX Claim 3; Page 91-95; 156pp; English.

XX The amino acid sequence of the novel N-methyl-D-aspartate (NMDA)
 receptor 1A (NMDAR1A). The NMDA receptor contains a second subunit
 selected from the subunits 2A (AAQ79375), 2B (AAQ79377), 2C (AAQ79372)
 and 2D (AAQ79378). The receptor forms part of a family of NMDA receptors
 which have cation-selective channels and bind glutamate and NMDA. The
 NMDAR1A gene was obtained from a cDNA library derived from human
 hippocampal tissue RNA using probes corresponding to sequences in the rat
 NMDAR1A receptor cDNA. 8 clones were isolated. The full length cDNA
 encoding the R1A receptor was generated by ligating the 2.1 kb
 ECORI-HindIII fragment from clone NMDA11 (AAQ79385), containing the 5'
 portion of the gene, with the 3.3 kb BglII-EcoRI fragment of clone NMDA10
 (AAQ79384), containing the 3' portion of the gene. The fragments were
 ligated into the plasmid pcDNA1. The resultant clone NMDAR1A contains 261
 bp of 5' untranslated DNA, the entire coding region for the NMDAR1A
 receptor and 1220 bp of 3' untranslated DNA. Based on the sequence of
 the 8 clones, derived from screening the library, a series of variants

Search completed: November 1, 2001, 16:24:54
Time: 49 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 1, 2001, 16:24:05 ; Search time 14.37 seconds
(without alignments)
588.405 Million cell updates/sec

Title: US-09-652-345-6
Perfect score: 543
Sequence: 1 IILLVSDHDEGRAAKRLET.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

num DB seq length: 0

num DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	100.0	885	2 JN0339	N-methyl-D-aspartate
2	543	100.0	901	2 JN0337	N-methyl-D-aspartate
3	543	100.0	922	2 JN0338	N-methyl-D-aspartate
4	543	100.0	938	2 S19710	N-methyl-D-aspartate
5	540	99.4	938	2 S21104	N-methyl-D-aspartate
6	538	99.1	938	2 A46612	N-methyl-D-aspartate
7	524	96.5	965	2 I51244	N-methyl-D-aspartate
8	522.5	96.2	906	2 A46296	N-methyl-D-aspartate
9	522.5	96.2	906	2 JN0341	N-methyl-D-aspartate
10	522.5	96.2	922	2 JN0340	N-methyl-D-aspartate
11	522.5	96.2	959	2 JN0336	N-methyl-D-aspartate
12	517.5	95.3	943	2 A47551	N-methyl-D-aspartate
13	184.5	34.0	997	2 S37554	glutamate receptor
14	119	21.9	950	2 T51134	ionotropic glutamate
15	119	21.9	953	2 E84732	probable ligand-ga
16	111.5	20.5	1012	2 T13603	probable N-methyl-
17	107	19.7	941	2 T51135	ligand-gated chann
18	107	19.7	962	2 D86186	hypothetical prote
19	101	18.6	976	2 T51137	ionotropic glutama
20	98	18.0	1039	2 T45779	probable glutamate
21	97.5	18.0	925	2 T51133	ligand gated chann
22	97.5	18.0	951	2 T51132	probable glutamate
23	97.5	18.0	975	2 A84550	probable ligand-ga
24	95.5	17.6	912	2 T51131	ligand gated chann
25	94	17.3	795	2 T20939	hypothetical prote
26	92.5	17.0	1323	2 T178557	N-methyl-D-asparta
27	92.5	17.0	1323	2 S27224	N-methyl-D-asparta
28	90.5	16.7	1356	1 C45219	N-methyl-D-asparta
29	88.5	16.3	920	2 B84640	probable ligand-ga

ALIGNMENTS

RESULT 1

JN0339
N-methyl-D-aspartate receptor 1 precursor, splice form E - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000
C:Accession: JN0339
R:Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 185, 826-832, 1992
A:Title: Structures and properties of seven isoforms of the NMDA receptor generated b
A:Reference number: JN0336; MUID:92328785
A:Accession: JN0339
A:Molecule type: mRNA
A:Residues: 1-885 <MOR>
A:Note: neither amino acid nor nucleotide sequence is complete
C:Comment: This protein plays a key role in memory acquisition, learning and neurolog
C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-885/Product: N-methyl-D-aspartate receptor 1E #status predicted <MAT>
F:427-848/Domain: glutamate receptor homology <GRH>
F:562-580/Domain: transmembrane #status predicted <TM1>
F:600-620/Domain: transmembrane #status predicted <TM2>
F:631-649/Domain: transmembrane #status predicted <TM3>
F:813-833/Domain: transmembrane #status predicted <TM4>
F:61,203,239,276,300,350,368,440,471,491,875/Binding site: carbohydrate (Asn) (coval
F:593,676,688,741,766/Binding site: phosphate (Ser) (covalent) #status predicted
F:683/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 543; DB 2; Length 885;
Best Local Similarity 100.0%; Pred. No. 4.2e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLERESKAEKVLQFDGCTKNVTALLMEARELEARVILS 60
|||||
Db 163 IILLVSDHDEGRAAKRLETLLERESKAEKVLQFDGCTKNVTALLMEARELEARVILS 222

QY 61 ASDDATATYRAAAMLNMTSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
|||||
Db 223 ASDDATATYRAAAMLNMTSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 2

JN0337
N-methyl-D-aspartate receptor 1 precursor, splice form C - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000
C:Accession: JN0337
R:Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 185, 826-832, 1992
A:Title: Structures and properties of seven isoforms of the NMDA receptor generated b

A:Reference number: JN0336; MUID:92328785
A:Accession: JN0337
A:Molecule type: mRNA
A:Residues: 1-901 <MOR>
A:Note: neither amino acid nor nucleotide sequence is complete
C:Comment: This protein plays a key role in memory acquisition, learning and neurologic
C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-901/Product: N-methyl-D-aspartate receptor 1C #status predicted <MAT>
F:427-848/Domain: glutamate receptor homology <GRH>
F:562-580/Domain: transmembrane #status predicted <TM1>
F:600-620/Domain: transmembrane #status predicted <TM2>
F:631-649/Domain: transmembrane #status predicted <TM3>
F:813-833/Domain: transmembrane #status predicted <TM4>
F:61-203,239,276,300,368,440,471,491/Binding site: carbohydrate (Asn) (covalent) #st
F:676,688,741,766/Binding site: phosphate (Ser) (covalent) #status predicted
F:676/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 543; DB 2; Length 901;
Best Local Similarity 100.0%; Pred. No. 4.3e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLEERESKAQKVLQDPGKNTVALLMEARELEAVIILS 60
|||||
DB 163 IILLVSDHDEGRAAKRLETLLEERESKAQKVLQDPGKNTVALLMEARELEAVIILS 222
|||||

QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
|||||
DB 223 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273
|||||

RESULT 3
JN0338
N-methyl-D-aspartate receptor 1 precursor, splice form D - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000
C:Accession: JN0338
R:Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 185, 826-832, 1992
A:Title: Structures and properties of seven isoforms of the NMDA receptor generated by a
A:Reference number: JN0336; MUID:92328785
A:Molecule type: mRNA
A:Residues: 1-922 <MOR>
A:Note: neither amino acid nor nucleotide sequence is complete
C:Comment: This protein plays a key role in memory acquisition, learning and neurologic
C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-922/Product: N-methyl-D-aspartate receptor 1D #status predicted <MAT>
F:427-848/Domain: glutamate receptor homology <GRH>
F:562-580/Domain: transmembrane #status predicted <TM1>
F:600-620/Domain: transmembrane #status predicted <TM2>
F:631-649/Domain: transmembrane #status predicted <TM3>
F:813-833/Domain: transmembrane #status predicted <TM4>
F:61-203,239,276,300,368,440,471,491,912/Binding site: carbohydrate (Asn) (covalent)
F:593,676,688,741,766/Binding site: phosphate (Ser) (covalent) #status predicted
F:683/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 543; DB 2; Length 922;
Best Local Similarity 100.0%; Pred. No. 4.4e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLEERESKAQKVLQDPGKNTVALLMEARELEAVIILS 60
|||||
DB 163 IILLVSDHDEGRAAKRLETLLEERESKAQKVLQDPGKNTVALLMEARELEAVIILS 222
|||||

QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
|||||

|||||
DB 223 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273
|||||

RESULT 4
S19710
N-methyl-D-aspartate receptor chain NMDA-R1A (alternatively spliced) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S19710; B46168
R:Moriyoshi, K.; Masu, M.; Ishii, T.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
Nature 354, 31-37, 1991
A:Title: Molecular cloning and characterization of the rat NMDA receptor.
A:Reference number: S19710; MUID:92049750
A:Accession: S19710
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-938 <MOR>
A:Cross-references: EMBL:X63255; NID:g57847; PIDN:CAA44914.1; PID:g57848
R:Nakanishi, N.; Axel, R.; Shneider, N.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 8552-8556, 1992
A:Title: Alternative splicing generates functionally distinct N-methyl-D-aspartate re
A:Reference number: A46168; MUID:92409554
A:Accession: B46168
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-938 <NAK>
A:Note: sequence extracted from NCBI backbone (NCBIP:113945)
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: phosphoprotein; transmembrane protein
F:427-848/Domain: glutamate receptor homology <GRH>

Query Match 100.0%; Score 543; DB 2; Length 938;
Best Local Similarity 100.0%; Pred. No. 4.5e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLEERESKAQKVLQDPGKNTVALLMEARELEAVIILS 60
|||||
DB 163 IILLVSDHDEGRAAKRLETLLEERESKAQKVLQDPGKNTVALLMEARELEAVIILS 222
|||||

QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
|||||
DB 223 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273
|||||

RESULT 5
S21104
N-methyl-D-aspartate receptor zeta-1 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000
C:Accession: S21104
R:Yamazaki, M.; Mori, H.; Araki, K.; Mori, K.J.; Mishina, M.
FEBS Lett. 300, 39-45, 1992
A:Title: Cloning, expression and modulation of a mouse NMDA receptor subunit.
A:Reference number: S21104; MUID:92192280
A:Accession: S21104
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-938 <YAM>
A:Cross-references: GB:D10028; NID:g220412; PIDN:BAA00920.1; PID:g220413
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: phosphoprotein; transmembrane protein
F:427-848/Domain: glutamate receptor homology <GRH>

Query Match 99.4%; Score 540; DB 2; Length 938;
Best Local Similarity 99.1%; Pred. No. 8.6e-43;
Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLEERESKAQKVLQDPGKNTVALLMEARELEAVIILS 60
|||||
DB 163 IILLVSDHDEGRAAKRLETLLEERESKAQKVLQDPGKNTVALLMEARELEAVIILS 222
|||||

QY 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
|||||
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 6
A46612
N-methyl-D-aspartate receptor chain 1 precursor, splice form 3 - human
N:Alternate names: N-methyl-D-aspartate glutamate receptor channel; NMDAR1
N:Contains: N-methyl-D-aspartate receptor 1 precursor splice form 2
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A46612; A59066; B59066
R:Karp, S.J.; Masu, M.; Ekl, T.; Ozawa, K.; Nakanishi, S.
J. Biol. Chem. 268, 3728-3733, 1993
A:Title: Molecular cloning and chromosomal localization of the key subunit of the human
A:Reference number: A46612; MUID:93155233
A:Accession: A46612
A:Molecule type: mRNA
A:Residues: 1-938 <KAR>
A:Cross-references: GB:D13515; NID:g219919; PIDN:BAA02732.1; PID:g219920
A:Experimental source: brain
R:Foldes, R.L.; Rampersad, V.; Kamboj, R.K.
Gene 131, 293-298, 1993
A:Title: Cloning and sequence analysis of cDNAs encoding human hippocampus N-methyl-D-as
A:Reference number: JN0838; MUID:94010324
A:Accession: A59066
A:Molecule type: mRNA
A:Residues: 300-863, 901-938 <FOLL>
A:Cross-references: GB:L13267; NID:g292284; PIDN:AAA36198.1; PID:g292285
A:Experimental source: hippocampus
A:Accession: B59066
A:Molecule type: mRNA
A:Residues: 11-935, 'T', 937-938 <FOLL2>
A:Cross-references: GB:L13268; NID:g292286; PIDN:AAB59361.1; PID:g292287
A:Experimental source: hippocampus
A:Note: sequence extracted from GenBank; the codons given for 488-Lys (GAG) and 936-Arg
C:Comment: This receptor is a member of the family of glutamate-gated ion channels. It i
e, neuronal degeneration, and neuronal cell death.
C:Comment: For other alternative splice forms, see PIR:A47551.
C:Genetics:
A:Gene: GDB:GRIN1; NMDAR1
A:Cross-references: GDB:L34707; OMIM:138249
A:Map position: 9q34.3-q34.3
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; receptor; transmembrane
F:1-938/Product: N-methyl-D-aspartate receptor 1 precursor splice form 3 #status predict
F:1-863, 901-938/Product: N-methyl-D-aspartate receptor 1 precursor splice form 3 #status
F:1-868/Domain: signal sequence #status predicted <Sig>
F:868-848/Domain: glutamate receptor homology <GRH>
F:862-580/Domain: transmembrane #status predicted <TRM1>
F:600-620/Domain: transmembrane #status predicted <TRM2>
F:631-649/Domain: transmembrane #status predicted <TRM3>
F:813-833/Domain: transmembrane #status predicted <TRM4>
F:61,203,239,276,300,350,368,440,471,491,771/Binding site: carbohydrate (Asn) (covalent)
F:593,687,713/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pre
F:676,741/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predict
F:681,711/Binding site: phosphate (Tyr) (covalent) #status predicted
F:683/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:748/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F:766/Binding site: phosphate (Ser) (covalent) (by CAMP- and CGMP-dependent kinases) #st

Query Match 99.1%; Score 538; DB 2; Length 938;
Best Local Similarity 98.2%; Pred. No. 1.3e-42;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILLVSDHDEGRAAKKRLTLLERESKAELVQDPGTKNVTALLMEARELEARVILS 60
|||||
Db 163 IILLVSDHDEGRAAKKRLTLLERESKAELVQDPGTKNVTALLMEARELEARVILS 222

QY 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
|||||
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 7
N-methyl-D-aspartate receptor type 1 - duck
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Jun-2000
C:Accession: I51244
R:Kurosawa, N.; Kondo, K.; Kimura, N.; Ikeda, T.; Tsukada, Y.
Neurochem. Res. 19, 575-580, 1994
A:Title: Molecular cloning and characterization of avian N-methyl-D-aspartate recepto
A:Reference number: I51244; MUID:94344315
A:Accession: I51244
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-965 <KUR>
A:Cross-references: GB:D83352; NID:g1199922; PIDN:BAA11898.1; PID:g1199923; GB:S71540
C:Superfamily: glutamate receptor; glutamate receptor homology
F:427-846/Domain: glutamate receptor homology <GRH>

Query Match 96.5%; Score 524; DB 2; Length 965;
Best Local Similarity 92.8%; Pred. No. 2.8e-41;
Matches 103; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILLVSDHDEGRAAKKRLTLLERESKAELVQDPGTKNVTALLMEARELEARVILS 60
|||||
Db 163 IILLVSDHDEGRAAKKRLTLLERESKAELVQDPGTKNVTALLMEARELEARVILS 222

QY 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
|||||
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 8
A46296
N-methyl-D-aspartate receptor (NMDAR1) splice form NR1b - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C:Accession: A46296
R:Durand, G.M.; Gregor, P.; Zheng, X.; Bennett, M.V.; Uhl, G.R.; Zukin, R.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 9359-9363, 1992
A:Title: Cloning of an apparent splice variant of the rat N-methyl-D-aspartate recept
A:Reference number: A46296; MUID:93028464
A:Accession: A46296
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-906 <DUR>
A:Cross-references: GB:S46394; GB:L01632; NID:g257305; PIDN:AAB23610.1; PID:g257306
A:Experimental source: ventral midbrain
A:Note: sequence extracted from NCBI backbone (NCBIN:116057, NCBIN:116064, NCBIP:1160
C:Superfamily: glutamate receptor; glutamate receptor homology
F:448-869/Domain: glutamate receptor homology <GRH>

Query Match 96.2%; Score 522.5; DB 2; Length 906;
Best Local Similarity 84.1%; Pred. No. 3.6e-41;
Matches 111; Conservative 0; Mismatches 0; Indels 21; Gaps 1;
QY 1 IILLVSDHDEGRAAKKRLTLLERESKAELVQDPGTKNVTALLMEARELEARVILS 39
|||||
Db 163 IILLVSDHDEGRAAKKRLTLLERESKAELVQDPGTKNVTALLMEARELEARVILS 222

QY 40 KNTALLMEARELEARVILSASEDDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRY 99
|||||
Db 223 KNTALLMEARELEARVILSASEDDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRY 282

QY 100 APDGIIGLQLIN 111
|||||
Db 283 APDGIIGLQLIN 294

RESULT 9

JN0341

N-methyl-D-aspartate receptor 1 precursor, splice form G - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000

C:Accession: JN0341

R:Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.

Biochem. Biophys. Res. Commun. 185, 826-832, 1992

A:Title: Structures and properties of seven isoforms of the NMDA receptor generated by a

A:Reference number: JN0336; MUID:92328785

A:Accession: JN0341

A:Molecule type: mRNA

A:Residues: 1-906 <MOR>

A>Note: neither amino acid nor nucleotide sequence is complete

C:Comment: This protein plays a key role in memory acquisition, learning and neurologiccal

C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.

C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.

C:Keywords: glutamate receptor; glutamate receptor homology

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; transmembrane protein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-906/Product: N-methyl-D-aspartate receptor 1G #status predicted <MAT>

F:448-869/Domain: glutamate receptor homology <CRM>

F:583-601/Domain: transmembrane #status predicted <TM1>

F:621-641/Domain: transmembrane #status predicted <TM2>

F:652-670/Domain: transmembrane #status predicted <TM3>

F:834-854/Domain: transmembrane #status predicted <TM4>

F:614, 697, 709, 762, 787/Binding site: phosphate (ser) (covalent) #status predicted

F:704/Binding site: phosphate (Thr) (covalent) #status predicted

```

Query Match      96.28; Score 522.5; DB 2; Length 906;
Best Local Similarity 84.18; Pred. No. 3,6e-41;
Matches 111; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

Oy 1 IILLVSDDHGGRRAQKRLFTLEERES-----KAEKYLPDPGT 39
      |||||
Db 163 IILLVSDDHGGRRAQKRLFTLEERESKKRNYNLDOLSYDNKRGRPAEKYLPDPGT 222
      |||||

Oy 40 KNYTALLMEARELEARYIILSASEDDAATVYRAAAMLNMTGSGYVWLVEERISGNALRY 99
      |||||
Db 223 KNYTALLMEARELEARYIILSASEDDAATVYRAAAMLNMTGSGYVWLVEERISGNALRY 282
      |||||

Oy 100 APDGIIGLOLIN 111
      |||||
Db 283 APDGIIGLOLIN 294
      |||||

RESULT 10
JN0340
N-methyl-D-aspartate receptor 1 precursor, splice form F - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Apr-1993 #sequence-revision 17-Apr-1993 #text_change 15-Sep-2000
C:Accession: JN0340
R:Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 185, 826-832, 1992
A:Title: Structures and properties of seven isoforms of the NMDA receptor generated by a
A:Reference number: JN0336; MUID:92328785
A:Accession: JN0340
A:Molecule type: mRNA
A:Residues: 1-922 <MOR>
C:Note: neither amino acid nor nucleotide sequence is complete
C:Comment: This protein plays a key role in memory acquisition, learning and neurologicc
C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-922/Product: N-methyl-D-aspartate receptor 1F #status predicted <MAT>
F:448-869/Domain: glutamate receptor homology <GHH>
F:583-601/Domain: transmembrane #status predicted <TM1>
F:621-641/Domain: transmembrane #status predicted <TM2>
F:652-670/Domain: transmembrane #status predicted <TM3>

```

F:834-854/Domain: transmembrane #status predicted <TM>
F:614,224,260,297,321,371,389,461,492,512/Binding site: carbohydrate (Asn) (covalently)
F:614,627,709,762,787/Binding site: phosphate (Ser) (covalently) #status predicted
F:704/Binding site: phosphate (Thr) (covalently) #status predicted

	Query Match	96.28;	Score 522.5;	DB 2;	Length 922;
	Best Local Similarity	84.18;	Pred. No. 3.7e-41;		
	Matches 111; Conservative	0;	Mismatches 0;	Indels 21;	Gaps
Oy	1 IILVSDDHESRAAKRLFTLLLEERES-----KAEKVQEPGPT 39				
Db	163 IILVSDDHEGRAAKRLFTLLLEERESKKRNYENDQLSYDNKRGPFAEKVLQFPDPT 222				
Oy	40 KNTVALMEARELEARVIITLSASDDDAATYVRAAAMLNMTGSGYVLVGEREISGNALRY 99				
Db	223 KNTVALMEARELEARVIITLSASDDDAATYVRAAAMLNMTGSGYVLVGEREISGNALRY 282				
Oy	100 APDGIIIGIQLIN 111				
Db	283 APDGIIIGIQLIN 294				

RESULT 11

JM0336

N-methyl-D-aspartate receptor 1 precursor, splice form B - rat

N.Alternate names: NMDA receptor RI-LL

C.Species: Rattus norvegicus (Norway rat)

C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000

C.Accession: JM0336, A46168; S23430

R.Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.

Biochem. Biophys. Res. Commun. 185, 826-832, 1992

A.Title: Structures and properties of seven isoforms of the NMDA receptor generated b

A.Reference number: JM0336; MUID: 92328785

A.Accession: JM0336

A.Molecule type: mRNA

A.Residues: 1-959 <MOR>

A.Note: neither amino acid nor nucleotide sequence is complete

R.Nakanishi, N.; Axel, R.; Schneider, N.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 8552-8556, 1992

A.Title: Alternative splicing generates functionally distinct N-methyl-D-aspartate re

A.Reference number: A46168; MUID: 92409554

A.Accession: A46168

A.Status: preliminary

A.Molecule type: nucleic acid

A.Residues: 1-959 <NA>

A.Cross-references: GB:545121; NID:q256028; PIDN:AMB23357.1; PID:q256031

A.Note: sequence inconsistent with the nucleotide translation

R.Anantharam, V.; Panchal, R.G.; Wilson, A.; Kolchane, V.V.; Treisman, S.N.; Bayley,

FEBS Lett. 305, 27-30, 1992

A.Title: Combinatorial RNA splicing alters the surface charge on the NMDA receptor.

A.Reference number: S23430; MUID: 92339518

A.Accession: S23430

A.Status: preliminary; translation not shown

A.Molecule type: mRNA

A.Residues: 1-959 <NA>

A.Cross-references: EMBL:X65227; NID:q56764; PIDN:CAA6335.1; PID:q56765

C.Comment: This protein plays a key role in memory acquisition, learning, and neurolo

C.Comment: This protein mediates neuronal functions in glutamate neurotransmission.

C.Keywords: glutamate receptor; glycoprotein; phosphoprotein; transmembrane protein

F.1-18/Domain: signal sequence #status predicted <SIG>

F.19-959/Product: N-methyl-D-aspartate receptor 1B #status predicted <MAT>

F.448-869/Domain: glutamate receptor homology <GRH>

F.583-601/Domain: transmembrane #status predicted <TM1>

F.621-641/Domain: transmembrane #status predicted <TM2>

F.652-670/Domain: transmembrane #status predicted <TM3>

F.834-854/Domain: transmembrane #status predicted <TM4>

F.61,224,260,297,321,371,389,461,492,512/Binding site: carbohydrate (Asn) (covalent)

F.614,697,709,766,787/Binding site: phosphate (Ser) (covalent) #status predicted

F.704/Binding site: phosphate (Thr) (covalent) #status predicted

A:Accession: PC4039
A:Molecule type: DNA
A:Residues: 1-86 <ZIM>
A:Cross-references: EMBL:Z32772; NID:g807892
A:Note: the authors translated the codon CGC for residue 5 as Ala, TGC for residue 22
C:Note: This translation is not annotated in GenBank entry HSNMDAR1A, release 111.0
C:Comment: This receptor is a member of the family of glutamate-gated ion channels. I
e, neuronal degeneration, and neuronal cell death.
C:Comment: For other alternative splice forms, see PIR:A46612.
C:Genetics:
A:Gene: GDB:GRIN1; NMDAR1
A:Cross-references: GDB:134707; OMIM:138249
A:Map position: 9q34.3-q34.3
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; receptor; transmembr
F:1-190.212-884,922-943/Product: N-methyl-D-aspartate receptor 1 precursor splice for
F:1-190.212-943/Product: N-methyl-D-aspartate receptor 1 precursor splice form 4 #sta
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-943/Product: N-methyl-D-aspartate receptor 1 #status predicted <MAT>
F:448-869/Domain: glutamate receptor homology <GRH>
F:583-601/Domain: transmembrane #status predicted <TRM1>
F:621-641/Domain: transmembrane #status predicted <TRM2>
F:652-670/Domain: transmembrane #status predicted <TRM3>
F:834-854/Domain: transmembrane #status predicted <TRM4>
F:61.224,260,297,321,371,389,461,492,512,933/Binding site: carbohydrate (Asn) (coval
F:614,708,734/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
F:697,762/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pred
F:702,732/Binding site: phosphate (Tyr) (covalent) #status predicted
F:704/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict
F:769/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict
F:787/Binding site: phosphate (Ser) (covalent) (by CAMP- and cGMP-dependent kinases)

Query Match 95.3%; Score 517.5; DB 2; Length 943;
Best Local Similarity 82.6%; Pred. No. 1.1e-40;
Matches 109; Conservative 2; Mismatches 0; Indels 21; Gaps 1;
Qy 1 IILLVSDDHGEGRAAQRLETLLEERES-----KAERVLQFDPGT 39
Db 163 IILLVSDDHGEGRAAQRLETLLEERESKKNRYENLDQLSYDNKRGPKAERVLPDGT 222
Qy 40 KNTVALLMEARELEARVILISASDDDAATVYRAAAMLNMTGSGYVWLVEREISGNALRY 99
Db 223 KNTVALLMEAKELEARVILISASDDDAATVYRAAAMLNMTGSGYVWLVEREISGNALRY 282
Qy 100 APDGIIGLQLIN 111
Db 283 APDGIIGLQLIN 294
RESULT 13
S33754
glutamate receptor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S33754
R:Ultsch, A.; Schuster, C.M.; Laube, B.; Betz, H.; Schmitt, B.
FEBS Lett. 324, 171-177, 1993
A:Title: Glutamate receptors of Drosophila melanogaster. Primary structure of a putat
A:Reference number: S33754; MUID:93285330
A:Accession: S33754
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-997 <ULT>
A:Cross-references: EMBL:X71790; NID:g312197; PIDN:CAA50675.1; PID:g312198
C:Genetics:
A:Gene: FlyBase:Nmdar
A:Cross-references: FlyBase:FBgn0010399
C:Superfamily: glutamate receptor; glutamate receptor homology
C:Keywords: neurotransmitter receptor
F:437-867/Domain: glutamate receptor homology <GRH>

[illegible]

```

Db      183  VVA1FEVDEYGRNCISVLGDALAKRAKISYKAFPGADNSSISDLLAVNLMESRIFV 242
QY      59  LSASEDDAATYVRAAAMINNTGSGYVH, 86
       :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db      243  VHNPDGSLNIFSVAKSIGMGSYVMI 270

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Search completed: November 1, 2001, 16:25:15
Job time: 70 sec

[illegible]

	Query Match	21.9%	Score 119;	DB 2;	Length 953;
	Best Local Similarity	28.4%;	Pred. No. 0.0027;		
	Matches 25; Conservative	17;	Indels 44;	Gaps 2;	1.
OY	1 IILVSDDEHGAAKRLLETLLEESKAQKLQDDPGTKN--VALMLAELELERRVII	58			
	::: : :: : : :: :	:			

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2001, 16:24:30 ; Search time 21 seconds
(without alignments)
699,327 Million cell updates/sec

Title: US-09-652-345-6
Perfect score: 543
Sequence: 1 IILLVSDHGGRAAQRLET.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL16:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Hit No.	Score	Query Match	Length	ID	Description
1	543	100.0	938	11 Q62683	Q62683 rattus norv
2	539	99.3	243	6 O19067	O19067 sus scrofa
3	524	96.5	965	13 Q91979	Q91979 anas platyr
4	522.5	96.2	922	11 Q62646	Q62646 rattus norv
5	522.5	96.2	943	11 Q62648	Q62648 rattus norv
6	517.5	95.3	906	4 Q9UPF9	Q9UPF9 homo sapien
7	517.5	95.3	943	4 Q9UPF8	Q9UPF8 homo sapien
8	462.5	85.2	904	13 Q91977	Q91977 xenopus lae
9	447.5	82.4	195	4 Q12868	Q12868 homo sapien
10	415	76.4	966	13 Q93338	Q93338 apteronotus
11	184.5	34.0	997	5 Q24418	Q24418 drosophila
12	180	33.1	126	13 Q91804	Q91804 xenopus lae
13	119	21.9	950	10 Q9SW97	Q9SW97 arabidopsis
14	119	21.9	953	10 Q9ZV67	Q9ZV67 arabidopsis
15	111.5	20.5	604	5 Q9W582	Q9W582 drosophila
16	111.5	20.5	1012	5 Q76903	Q76903 drosophila
17	107	19.7	941	10 Q9SWD9	Q9SWD9 arabidopsis
18	107	19.7	962	10 Q23048	Q23048 arabidopsis
19	102.5	18.9	1336	4 O15399	O15399 homo sapien

20	98	18.0	1039	10 Q9SD01	Q9SD01 arabidopsis
21	97.5	18.0	925	10 Q49119	Q49119 arabidopsis
22	97.5	18.0	951	10 Q9ZT36	Q9ZT36 arabidopsis
23	97.5	18.0	975	10 Q22738	Q22738 arabidopsis
24	95.5	17.6	912	10 Q9SES5	Q9SES5 brassica na
25	94	17.3	795	5 Q22063	Q22063 caenorhabdi
26	92.5	17.0	1323	11 Q62645	Q62645 rattus norv
27	92.5	17.0	1323	11 Q63381	Q63381 rattus norv
28	92.5	17.0	1323	11 Q63382	Q63382 rattus norv
29	92.5	17.0	1356	11 Q63729	Q63729 rattus norv
30	88.5	16.3	920	10 Q9SHV1	Q9SHV1 arabidopsis
31	87	16.0	921	10 Q9SDQ4	Q9SDQ4 arabidopsis
32	87	16.0	923	10 Q9ZV68	Q9ZV68 arabidopsis
33	86.5	15.9	925	10 Q65498	Q65498 arabidopsis
34	86	15.8	867	10 Q9LV72	Q9LV72 arabidopsis
35	84.5	15.6	860	10 Q9FH75	Q9FH75 arabidopsis
36	81	14.9	1482	11 Q62684	Q62684 rattus norv
37	81	14.9	1484	4 Q12919	Q12919 homo sapien
38	81	14.9	1484	4 Q13224	Q13224 homo sapien
39	81	14.9	1484	4 Q9UM56	Q9UM56 homo sapien
40	79.5	14.6	940	13 Q73635	Q73635 fugu rubrip
41	78.5	14.5	1236	4 O15398	O15398 homo sapien
42	78	14.4	814	5 Q9VEJ2	Q9VEJ2 drosophila
43	78	14.4	1464	4 Q12879	Q12879 homo sapien
44	78	14.4	1464	11 O08948	O08948 rattus norv
45	77.5	14.3	858	10 Q9SRR4	Q9SRR4 arabidopsis

ALIGNMENTS

RESULT 1

Q62683 ID Q62683 PRELIMINARY; PRT; 938 AA.

AC Q62683;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NMDAR1 GLUTAMATE RECEPTOR SUBUNIT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Sullivan J.M., Traynelis S.F., Chen H., Escobar W., Heinemann S.F.,
RA Lipton S.A.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U11418; AAA19659.1; -.
DR HSSP; Q05586; 2NRI.
DR InterPro; IPR001311; -.
DR InterPro; IPR001320; -.
DR InterPro; IPR001508; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR001828; -.
DR Pfam; PF00060; lig_chan; 1.
DR PRINTS; PR001094; ANF_receptor; 1.
DR SMART; SM00079; PSPE; 1.
SQ SEQUENCE 938 AA; 105568 MW; 3B279C4925AF16DE CRC64;

Query Match 100.0%; Score 543; DB 11; Length 938;
Best Local Similarity 100.0%; Pred. No. 2.4e-42;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	IILLVSDHGGRAAQRLETLLERESKAKVLOFDPGCKNVNTALLMEAREARVILS 60		
Db	163	IILLVSDHGGRAAQRLETLLERESKAKVLOFDPGCKNVNTALLMEAREARVILS 222		
QY	61	ASEDDAATVYRAAAMLMNTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111		
Db	223	ASEDDAATVYRAAAMLMNTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273		


```
RESULT 2
O19067 ID O19067 PRELIMINARY; PRT; 243 AA.
AC O19067:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE N-METHYL-D-ASPARTATE RECEPTOR (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RQ TISSUE=HYPOTHALAMUS;
RZ Matteri R.L.;
R1 Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF008560; AAB63295.1; -.
DR InterPro; IPR001828; -.
DR Pfam; PF01094; ANF_receptor; 1.
FT NON_TER 1 243
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 27122 MW; 910EA8342DB06DDF CRC64;

Query Match 99.3%; Score 539; DB 6; Length 243;
Best Local Similarity 99.1%; Pred. No. 1e-42; Indels 0; Gaps 0;
Matches 110; Conservative 1; Mismatches 0;

QY 1 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPKNTVALLMEARELEARVILS 60
DB 54 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPKNTVALLMEARELEARVILS 113
QY 61 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
DB 114 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 164

RESULT 3
O91979 ID O91979 PRELIMINARY; PRT; 965 AA.
AC O91979:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE N-METHYL-D-ASPARTATE RECEPTOR TYPE1 PRECURSOR.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RQ kimura N.;
R1 Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83352; BAA11898.1; -.
DR HSSP; Q05586; 2NR1.
DR InterPro; IPR001311; -.
DR InterPro; IPR001320; -.
DR InterPro; IPR001508; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR001828; -.
DR Pfam; PF00060; lig_chan; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00177; NMDARECEPTOR.
SQ SEQUENCE 922 AA; 103880 MW; 847CEED410182B5C CRC64;

Query Match 96.2%; Score 522.5; DB 11; Length 922;
Best Local Similarity 84.1%; Pred. No. 1.9e-40;
Matches 111; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPKNTVALLMEARELEARVILS 39
DB 163 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPKNTVALLMEARELEARVILS 222
QY 40 KNTVALLMEARELEARVILSASEDDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRY 99
DB 223 KNTVALLMEARELEARVILSASEDDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRY 282
QY 100 APDGIIGLQLIN 111
```

Db 283 APDGIIGLQLIN 294
|||||

RESULT 5
Q62648 PRELIMINARY; PRT; 943 AA.

AC Q62648;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 15, Last annotation update)
DE N-METHYL-D-ASPARTATE RECEPTOR NMDAR1-3B SUBUNIT.
GN NMDAR1.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN=SPRAGUE-DAWLEY; TISSUE=FOREBRAIN;

RX MEDLINE=93264089; PubMed=7684237;

RA Hollmann M., Boulter J., Maron C., Beasley L., Sullivan J., Pecht G.,
Heinemann S.;

"zinc potentiates agonist-induced currents at certain splice variants
of the NMDA receptor.";
RL Neuron 10:943-954(1993).

RN [2]

SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=FOREBRAIN;

RA Boulter J.;

RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; U08266; AAB50931.1; -.

DR HSSP; Q05586; 2NRI.

DR InterPro; IPR001311; -.

DR InterPro; IPR001320; -.

DR InterPro; IPR001508; -.

DR InterPro; IPR001622; -.

DR InterPro; IPR001828; -.

DR Pfam; PF00060; lig_chan; 1.

DR Pfam; PF01094; ANF_receptor; 1.

DR PRINTS; PR00177; NMDARECEPTOR.

DR SMART; SM00079; PBPe; 1.

SQ SEQUENCE 943 AA; 106150 MW; 3D521E349A5741BB CRC64;

Query Match 96.2%; Score 522.5; DB 11; Length 943;

Best Local Similarity 84.1%; Pred. No. 2e-40;

Matches 111; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 IILLVSDHDEGAAQKRLTLEERES-----KAEKVLQFDPGT 39
|||||

Db 163 IILLVSDHDEGAAQKRLTLEERESKSKRNVENLDQLSYDNKRGPKAEKVLQFDPGT 222
|||||

QY 40 KNTVALLMEARELEARVILSASEDDAATVYRAAAMLNTGSGYVWLVGEREISGNALRY 99
|||||

Db 223 KNTVALLMEARELEARVILSASEDDAATVYRAAAMLNTGSGYVWLVGEREISGNALRY 282
|||||

QY 100 APDGIIGLQLIN 111

Db 283 APDGIIGLQLIN 294

RESULT 6

Q9UPF9

ID Q9UPF9 PRELIMINARY; PRT; 906 AA.

AC Q9UPF9;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE NMDAR1 SUBUNIT ISOFORM 3B.

GN HNMAR1-3B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=97375389; PubMed=9231706;

RA Nash N.R., Hellman C.J., Rees H.D., Levey A.I.;

RT "Cloning and localization of exon 5-containing isoforms of the NMDAR1
subunit in human and rat brains.";

RL J. Neurochem. 69:485-493(1997).

DR EMBL; AF015730; AAB67723.1; -.

DR HSSP; Q05586; 2NRI.

DR InterPro; IPR001311; -.

DR InterPro; IPR001320; -.

DR InterPro; IPR001508; -.

DR InterPro; IPR001622; -.

DR InterPro; IPR001828; -.

DR Pfam; PF00060; lig_chan; 1.

DR Pfam; PF01094; ANF_receptor; 3.

DR PRINTS; PR00177; NMDARECEPTOR.

DR SMART; SM00079; PBPe; 1.

SQ SEQUENCE 906 AA; 101884 MW; 76199662AE0F313A CRC64;

Query Match 95.3%; Score 517.5; DB 4; Length 906;

Best Local Similarity 82.6%; Pred. No. 5.6e-40;

Matches 109; Conservative 2; Mismatches 0; Indels 21; Gaps 1;

QY 1 IILLVSDHDEGAAQKRLTLEERES-----KAEKVLQFDPGT 39
|||||

Db 163 IILLVSDHDEGAAQKRLTLEERESKSKRNVENLDQLSYDNKRGPKAEKVLQFDPGT 222
|||||

QY 40 KNTVALLMEARELEARVILSASEDDAATVYRAAAMLNTGSGYVWLVGEREISGNALRY 99
|||||

Db 223 KNTVALLMEARELEARVILSASEDDAATVYRAAAMLNTGSGYVWLVGEREISGNALRY 282
|||||

QY 100 APDGIIGLQLIN 111

Db 283 APDGIIGLQLIN 294

RESULT 7

Q9UPF8

ID Q9UPF8 PRELIMINARY; PRT; 943 AA.

AC Q9UPF8;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE NMDAR1 SUBUNIT ISOFORM 4B.

GN HNMAR1-4B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=97375389; PubMed=9231706;

RA Nash N.R., Hellman C.J., Rees H.D., Levey A.I.;

RT "Cloning and localization of exon 5-containing isoforms of the NMDAR1
subunit in human and rat brains.";

RL J. Neurochem. 69:485-493(1997).

DR EMBL; AF015731; AAB67724.1; -.

DR HSSP; Q05586; 2NRI.

DR InterPro; IPR001311; -.

DR InterPro; IPR001320; -.

DR InterPro; IPR001508; -.

DR InterPro; IPR001622; -.

DR InterPro; IPR001828; -.

DR Pfam; PF00060; lig_chan; 1.

DR Pfam; PF01094; ANF_receptor; 3.

DR PRINTS; PR00177; NMDARECEPTOR.

DR SMART; SM00079; PBPe; 1.

SQ SEQUENCE 943 AA; 106048 MW; 90905DD81BE7FE69 CRC64;

Query Match		95.3%	Score 517.5;	DB 4;	Length 943;
Best Local Similarity		82.6%	Pred. No. 5.9e-40;	Mismatches 0;	Indels 21; Gaps
Matches 109;	Conservative	2;			
QY	1 IILLVSDDHGGRAAQRKLETLLES-	-	-	-	-KAENVLQDPGT 39
Db	IILVVDDHGGRAAQRKLETLLES				
Db	163 IILLVSDDHGGRAAQRKLETLLES	SKKRNYENLDQLSYDNKRGPKAEKVLPDPTG	222		
QY	40 KNTATLLMEARELEARVIILSASEDDAAVTYRAAALNMTGSYVLWGERETSGNALRY	99			
Db	KNTALLMEAKELEARVIILSASEDDAAVTYRAAALNMTGSYVLWGERETSGNALRY	282			
QY	100 APDGIIIGLQLIN 111				
Db	283 APDGIIIGLQLIN 294				
R	FILT 8				
ID	Q91977 PRELIMINARY;	PRT;	904 AA.		
AC	Q91977; Q91805;				
DT	01-NOV-1996 (TrEMBLrel. 01, Created)				
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)				
DE	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)				
DE	NMDA GLUTAMATE RECEPTOR SUBUNIT PRECURSOR (NMDA RECEPTOR).				
GN	NR1.				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	TISSUE-BRAIN;				
RX	MEDLINE=97115781; PubMed=8955083;				
RA	Soloviev M.M., Brierley M.J., Shao Z.Y., Mellor I.R., Volkova T.M.,				
RA	Kamboj R., Ishimaru H., Sudan H., Harris J., Foldes R.L.,				
RA	Grishin E.V., Usherwood P.N.R., Barnard E.A.;				
RT	"Functional expression of a recombinant unitary glutamate receptor				
RT	from xenopus, which contains N-methyl-D-aspartate (NMDA) and non-NMDA				
RT	receptor subunits.";				
J	J. Biol. Chem. 271:32572-32579(1996).				
RN	[2]				
R	SEQUENCE OF 79-225 FROM N.A.				
R	TISSUE-BRAIN:				
R	Soloviev M.M.;				
RL	Submitted (Aug-1996) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; X94156; CAA63871.1; -				
DR	EMBL; X94081; CAA63825.1; -				
DR	EMBL; X99885; CAA68167.1; -				
DR	HSP; Q05586; 2NR1.				
DR	InterPro; IPRO01311; -				
DR	InterPro; IPRO01320; -				
DR	InterPro; IPRO01508; -				
DR	InterPro; IPRO01622; -				
DR	InterPro; IPRO01828; -				
DR	Pfam; PF00060; lig_chan; 1.				
DR	Pfam; PF01094; ANF_receptor; 1.				
DR	SMART; PR00177; NMDARECEPTOR.				
DR	SMART; SM00079; PBPe; 1.				
KW	SIGNAL.				
FT	SIGNAL	1	20	POTENTIAL.	
FT	CHAIN	21	904		
SEQ	SEQUENCE	904 AA;	101893 MW;	46D8FE0EA6D903F2 CRC64;	
Query Match		85.2%	Score 462.5;	DB 13;	Length 904;
Best Local Similarity		71.2%	Pred. No. 7.5e-35;	Mismatches 3;	Indels 21; Gaps
Matches 94;	Conservative	14;			
QY	1 IILLVSDDHGGRAAQRKLETLLES-	-	-	-	-KAENVLQDPGT 39
	: :	:	:	:	: :

Db	180	VVAIFVDDEYGRNGISVIGDALAKKRAKTSYKRAA	PPGADN	SSISD	LLASV	NLM	ESRIFV	233
QY	59	LSASEDDAATVYRAAAMLNNTGGYVWL	86					
Db	240	VHVNPD	SGLNIF	SVAKSL	GMGSGY	YWI	267	
RESULT 14								
Q92V67								
ID	Q92V67	PRELIMINARY;	PRT;	953	AA.			
AC	Q92V67;							
DT	01-MAY-1999	(TrEMBLrel. 10, Created)						
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)						
DT	01-MAR-2001	(TrEMBLrel. 16, Last annotation update)						
DE	PUTATIVE ION CHANNEL PROTEIN.							
GN	T32F6.9.							
OS	Arabidopsis thaliana (Mouse-ear cress).							
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;							
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;							
OC	Brassicales; Brassicaceae; Arabidopsids.							
OX	NCBI_TaxID=3702;							
OX	NCBI_TaxID=3702;							
RP	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=CV. COLUMBIA;							
RC	Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,							
RA	Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;							
RA	"Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence.;"							
RT	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.							
DR	EMBL; AC005700; AAC69939.1; -							
DR	InterPro; IPR001311; -							
DR	InterPro; IPR001320; -							
DR	InterPro; IPR001828; -							
DR	Pfam; PF00060; lig_chan; 1.							
DR	Pfam; PF01094; ANF_receptor; 1.							
DR	SMART; SM00079; PBPE; 1							
SQ	SEQUENCE 953 AA; 106810 MW; 9C13F10ECFF5116 CRC64;							
Query Match	21.9%;	Score	119;	DB	10;	Length	953;	
Best Local Similarity	28.4%;	Pred. NO.	0.0091;					
Matches	25;	Conservative	17;	Mismatches	44;	Indels	2;	Gaps
QY	1	IILLVSDH	EGRAQK	RLETL	LEERSK	AEKV	LFQD	PGTKN--VTALLMEARLEARVII 58
Db	183	VVAIFVDDEYGRNGISVIGDALAKKRAKTSYKRAA	PPGADN	SSISD	LLASV	NLM	ESRIFV	242
QY	59	LSASEDDAATVYRAAAMLNNTGGYVWL	86					
Db	243	VHVNPD	SGLNIF	SVAKSL	GMGSGY	YWI	270	
RESULT 15								
Q9W582								
ID	Q9W582	PRELIMINARY;	PRT;	604	AA.			
AC	Q9W582;							
DT	01-MAY-2000	(TrEMBLrel. 13, Created)						
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)						
DT	01-MAR-2001	(TrEMBLrel. 16, Last annotation update)						
DE	EG:80H7.7 PROTEIN.							
GN	EG:80H7.7 OR CG14793.							
OS	Drosophila melanogaster (Fruit fly).							
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;							
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;							
OC	Ephydroidea; Drosophilidae; Drosophila.							
OX	NCBI_TaxID=7227;							
OX	NCBI_TaxID=7227;							
RP	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=BERKELEY;							
RC	MEDLINE=20196006; PubMed=10731132;							
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,							
RA	Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,							
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,							

Search completed: November 1, 2001, 16:27:36
Job time: 186 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 1, 2001, 16:25:00 ; Search time 11.56 seconds
(without alignments)
328.924 Million cell updates/sec

Title: US-09-652-345-6
Perfect score: 543
Sequence: 1 IILVSDDEHRAAQKRLT.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543	100.0	938	1	NMZ1_RAT
2	540	99.4	938	1	P35438 mus musculus
3	538	99.1	938	1	NMZ1_HUMAN
4	92.5	17.0	1323	1	NME4_MOUSE
5	81	14.9	1482	1	NME2_MOUSE
6	81	14.9	1482	1	NME2_RAT
7	78.5	14.5	1233	1	NME3_HUMAN
8	78	14.4	1464	1	NME1_MOUSE
9	78	14.4	1464	1	NME1_RAT
10	77.5	14.3	1237	1	NME3_RAT
11	77.5	14.3	1239	1	NME3_MOUSE
12	75	13.8	956	1	GLK4_RAT
13	73.5	13.5	866	1	MYSP_SCHJA
14	72.5	13.4	240	1	PYRH_BACSU
15	72.5	13.4	1085	1	CASR_BOVIN
16	72	13.3	956	1	GLK4_HUMAN
17	70.5	13.0	321	1	RT01_YEAST
18	70.5	13.0	496	1	GTR3_CHICK
19	70.5	13.0	908	1	MGR8_HUMAN
20	70.5	13.0	908	1	MGR8_RAT
21	70	12.9	877	1	MGR6_HUMAN
22	69.5	12.8	344	1	STSY_RAUSE
23	69.5	12.8	908	1	MGR8_MOUSE
24	69	12.7	912	1	MGR4_HUMAN
25	69	12.7	979	1	GLK5_MOUSE
26	69	12.6	979	1	GLK5_RAT
27	68.5	12.6	507	1	PDI_DATGL
28	68.5	12.6	1078	1	CASR_HUMAN
29	68.5	12.6	1079	1	CASR_MOUSE
30	68.5	12.6	1079	1	CASR_RAT
31	68	12.5	836	1	GLK1_MOUSE
32	68	12.5	889	1	GLK2_MOUSE
33	68	12.5	908	1	GLK2_HUMAN

34	68	12.5	908	1	GLK2_RAT
35	68	12.5	918	1	GLK1_HUMAN
36	68	12.5	980	1	GLK5_HUMAN
37	67	12.3	417	1	PKGB_LEIME
38	67	12.3	499	1	XYLB_BACSU
39	67	12.3	866	1	MYSP_SCHMA
40	67	12.3	912	1	MGR4_RAT
41	67	12.3	2017	1	MYSN_DROME
42	66.5	12.2	458	1	CD4_MACFA
43	66.5	12.2	458	1	CD4_MACFU
44	66.5	12.2	458	1	CD4_MACMU
45	66.5	12.2	458	1	CD4_MACNE

ALIGNMENTS

RESULT	1
NMZ1_RAT	
ID	NMZ1_RAT
AC	P35439;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	GLUTAMATE [NMDA] RECEPTOR SUBUNIT ZETA 1 PRECURSOR (NR1) (NMD-R1)
DE	(N-METHYL-D-ASPARTATE RECEPTOR).
GN	GRIN1 OR NMDAR1.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=92049750; PubMed=1834949;
RA	Moriyoshi K., Masu M., Ishii T., Shigemoto R., Mizuno N.,
RA	Nakanishi S.;
RT	"Molecular cloning and characterization of the rat NMDA receptor.";
RL	Nature 354:31-37(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92409554; PubMed=1388270;
RA	Nakanishi N., Axel R., Shneider N.A.;
RT	"Alternative splicing generates functionally distinct N-methyl-D-
RT	aspartate receptors.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:8552-8556(1992).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Forebrain;
RX	MEDLINE=93264089; PubMed=7684237;
RA	Hollmann M., Boulter J., Maron C., Beasley L., Sullivan J., Pecht G.,
RA	Heinemann S.;
RT	"Zinc potentiates agonist-induced currents at certain splice variants
RT	of the NMDA receptor.";
RL	Neuron 10:943-954(1993).
RN	[4]
RP	SEQUENCE OF 1-86 FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX	MEDLINE=94002162; PubMed=8399301;
RA	Bal G., Kuslak J.W.;
RT	"Cloning and analysis of the 5' flanking sequence of the rat
RT	N-methyl-D-aspartate receptor 1 (NMDAR1) gene.";
RL	Biochim. Biophys. Acta 1152:197-200(1993).
RN	[5]
RP	ALTERNATIVE SPLICING.
RC	TISSUE=Brain;
RX	MEDLINE=92328785; PubMed=1352681;
RA	Sugihara H., Moriyoshi K., Ishii T., Masu M., Nakanishi S.;
RT	"Structures and properties of seven isoforms of the NMDA receptor
RT	generated by alternative splicing.";
RL	Biochem. Biophys. Res. Commun. 185:826-832(1992).
RN	[6]
RP	ALTERNATIVE SPLICING.

RC TISSUE=Brain;
RX MEDLINE=92339518; PubMed=1386026;
RA Anantharam V., Panchal R., Wilson A., Koltchin V.V.,
RT Treistman S.N., Bayley H.;
RT "Combinatorial RNA splicing alters the surface charge on the NMDA
RT receptor";
RL FEBS Lett. 305:27-30(1992).
CC -!- FUNCTION: NMDA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS
CC POSSESSES HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT
CC SENSITIVITY TO MAGNESIUM AND IS MODULATED BY GLYCINE. THIS PROTEIN
CC PLAYS A KEY ROLE IN SYNAPTIC PLASTICITY, SYNAPTOGENESIS,
CC EXCITOTOXICITY, MEMORY ACQUISITION AND LEARNING. IT MEDIATES
CC NEURONAL FUNCTIONS IN GLUTAMATE NEUROTRANSMISSION.
CC -!- SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT AND A ZETA SUBUNIT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 7 ISOFORMS; A (SHOWN HERE), B, C, D, E, F
CC AND G: ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- PTM: NMDA IS PROBABLY REGULATED BY C-TERMINAL PHOSPHORYLATION OF
CC AN ISOFORM OF NR1 BY PKC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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DR EMBL: D10028; BAA00920.1; -
DR PIR: S21104; S21104.
DR MGD; MGI:95819; Grin1.
DR InterPro: IPR001320; -
DR InterPro: IPR001508; -
DR InterPro: IPR001828; -
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00060; lig_chan; 1.
DR PRINTS; PR00177; NMDARECEPTOR.
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KW Ionic channel; Magnesium; Phosphorylation.
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FT DOMAIN 19 561
FT TRANSMEM 562 580
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FT DOMAIN 834 938
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QY 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273
ID HUMAN STANDARD; PRT; 938 AA.
AC Q05586; P35437.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GLUTAMATE [NMDA] RECEPTOR SUBUNIT ZETA 1 PRECURSOR (NR1).
GN GRIN1 OR NMDAR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93155233; PubMed=7679115;
RA Karp S.J., Masu M., Eki T., Ozawa K., Nakanishi S.;
RT "Molecular cloning and chromosomal localization of the key subunit of
the human N-methyl-D-aspartate receptor.";
J. Biol. Chem. 268:3728-3733(1993).
[2]
RP SEQUENCE FROM N.A.
RT TISSUE=Brain;

RX MEDLINE=93281695; PubMed=7685113;
RA Planells-Cases R., Sun W., Ferrer-Montiel A.V., Montal M.;
RT "Molecular cloning, functional expression, and pharmacological
characterization of an N-methyl-D-aspartate receptor subunit from
human brain.";
Proc. Natl. Acad. Sci. U.S.A. 90:5057-5061(1993).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94010324; PubMed=8406025;
RA Foldes R.L., Rampersad V., Kamboj R.K.;
RT "Cloning and sequence analysis of cDNAs encoding human hippocampus N-
methyl-D-aspartate receptor subunits: evidence for alternative RNA
splicing.";
Gene 131:293-298(1993).
[4]
RP SEQUENCE OF 364-464 FROM N.A.
RX MEDLINE=93211924; PubMed=7681588;
RA Youkin D.P., Tang C.-M., Hardy M., Reddy U.R., Shi Q.-Y.,
Pleasure S.J., Lee V.M.-Y., Pleasure D.;
RT "Inducible expression of neuronal glutamate receptor channels in the
NT2 human cell line.";
Proc. Natl. Acad. Sci. U.S.A. 90:2174-2178(1993).
[5]
RP PHOSPHORYLATION BY PKC.
RX MEDLINE=93302854; PubMed=8316301;
RA Tingley W.G., Roche K.W., Thompson A.K., Haganir R.L.;
RT "Regulation of NMDA receptor phosphorylation by alternative splicing
of the C-terminal domain.";
Nature 364:70-73(1993).
[6]
RP STRUCTURE BY NMR OF 599-631.
RA Gesell J.J.; University of Pennsylvania, U.S.A.
RL Thesis (1997); NMDA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS
CC -!- FUNCTION: NMDA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS
CC POSSESSES HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT
CC SENSITIVITY TO MAGNESIUM AND IS MODULATED BY GLYCINE. THIS PROTEIN
CC PLAYS A KEY ROLE IN SYNAPTIC PLASTICITY, SYNAPTIC ACQUISITION, IT MEDIATES
CC EXCITOTOXICITY, MEMORY ACQUISITION AND LEARNING. IT MEDIATES
CC NEURONAL FUNCTIONS IN GLUTAMATE NEUROTRANSMISSION.
CC -!- SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT AND A ZETA SUBUNIT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS: SHORT, MEDIUM AND LONG (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE C-
CC TERMINUS.
CC -!- PTM: NMDA IS PROBABLY REGULATED BY C-TERMINAL PHOSPHORYLATION OF
CC AN ISOFORM OF NR1 BY PKC.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.

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DR EMBL: D13515; BAA02732.1; -
DR EMBL: L05666; AAA21180.1; -
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DR EMBL: S57708; AAB25917.1; -
DR PIR: A46612; A46612.
DR PIR: JN0838; JN0838.
DR PDB: 138249; -
DR PDB; 2NR1; 29-APR-98.
DR MIM; 138249; -
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DR Pfam; PF00060; lig_chan; 1.
DR PRINTS; PR00177; NMDARECEPTOR.

[illegible][illegible]

[illegible]

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MEDLINE=92244361; PubMed=1374164;
Meguro H., Mori H., Araki K., Kushiya E., Kutsuwada T.,
Yamazaki M., Kumanishi T., Arakawa M., Sakimura K., Mishina M.;
"Functional characterization of a heteromeric NM2A receptor channel
expressed from cloned cDNAs.";
Nature 357:70-74(1992).
-1- FUNCTION: NM2A RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS
POSSESSES HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT
SENSITIVITY TO MAGNESIUM AND IS MEDIATED BY GLYCINE.
-1- SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT AND A ZETA SUBUNIT.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; D10217; BAA01069.1; -
PIR; S29159; S29159.
MGD; MGI:95820; Grin2a.
InterPro; IPR001320; -
Pfam; PF00060; lig_chan; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Calcium; Magnesium.
KW SIGNAL 1 22 POTENTIAL.
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FT EPSILON 1.
FT DOMAIN 23 556 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 557 576 1 (POTENTIAL).
FT TRANSMEM 599 619 2 (POTENTIAL).
FT TRANSMEM 629 654 3 (POTENTIAL).
FT TRANSMEM 817 837 4 (POTENTIAL).
FT SITE 614 614 FUNCTIONAL DETERMINANT OF NM2A
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FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
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Db 217 VOLKKIHSSVILVYCSKDEAVLLSEARSLGTGYDFEWIVPSL-VSGNTELIPIKFEPSG 275
QY 104 IIGL 107
Db 276 LISV 279
RESULT 9
NM2A_RAT
ID ID NM2A_RAT STANDARD; PRT; 1464 AA.
AC AC Q00959;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR (N-METHYL
D-ASPARTATE RECEPTOR SUBTYPE 2A) (NR2A) (NMDAR2A).
GN GRIN2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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KW Transferase: Kinase; Pyrimidine biosynthesis.
SQ SEQUENCE 240 AA; 25991 MW; 5D9DEF9AA36A29A9 CRC64;

Query Match
13.4%; Score 72.5; DB 1; Length 240;

Best Local Similarity 22.9%; Pred. No. 5.2;
Matches 25; Conservative 22; Mismatches 33; Indels 29; Gaps 3;
QY 3 LVSDDHEGRAAKRLETLLEERE-----SKAEKVLQDPGPKNV-----TA 44
DB 86 LALQDLETLIGSRVQSTIEMQVAEPYIRRAIRHLEKKRVVIFAAGTGNFYFSDTT 145
QY 45 LLMEARELEARVILSAS-----EDDAATVYRAAAMNMTGSG 82
DB 146 AALRAAEIADVILMAKNVGVYNADPRKDESAVYESLSYLDVLKDG 194

RESULT 15
CASR_BOVIN STANDARD; PRT: 1085 AA.
AC P35384;
DT 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
DE CELL CALCIUM-SENSING RECEPTOR).
GN CASR OR PCAR1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Parathyroid;
RX MEDLINE=94077182; PubMed=8255296;
RA Brown E.M., Gamba G., Riccardi D., Lombardi M., Butters R., Kifor O.,
RA Sun A., Hediger M.A., Lytton J., Hebert S.C.;
RT "Cloning and characterization of an extracellular Ca(2+)-sensing
RT receptor from bovine parathyroid."
RL Nature 366:575-580(1993).
CC -!- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; S67307; AAB29171.1; -.
CC PIR; S40476; S40476.
CC GCRD; GCR_0900; -.
CC InterPro: IPR000068; -.
CC InterPro: IPR000337; -.
CC InterPro: IPR001828; -.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PRINTS; PR00592; CASNSINGR.
CC PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
CC PROSITE; PS00981; G_PROTEIN_RECP_F3_4; 1.
CC PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 19
FT CHAIN 20 1085 EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
FT DOMAIN 20 613 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 614 636 I (POTENTIAL).
FT DOMAIN 637 650 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 651 671 II (POTENTIAL).
FT DOMAIN 672 682 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 683 701 III (POTENTIAL).
FT DOMAIN 702 725 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 726 746 IV (POTENTIAL).
FT DOMAIN 747 770 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 771 793 V (POTENTIAL).
FT DOMAIN 794 806 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 807 829 VI (POTENTIAL).
FT DOMAIN 830 837 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 838 863 VII (POTENTIAL).
FT DOMAIN 864 1085 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 542 542 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 595 595 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1085 AA; 121170 MW; 5D66DE8C9CD13E47 CRG64;

Query Match 13.4%; Score 72.5; DB 1; Length 1085;
Best Local Similarity 23.6%; Pred. No. 29;
Matches 29; Conservative 18; Mismatches 47; Indels 29; Gaps 4;
QY 4 LVSDDHEGRAAKRLETLLEERE-----SKAEKVLQDPGPKNVTTALLMEARE 51
DB 213 IAADDYGRPGIEKFEAEERDIDCFSELISQYSDEKIQQVVEVIONST----- 264
QY 52 LEARVILSASEDDAATVYRAAAMNMTGSGYVNLVGEREISGNALR-----YAPDGIIG 106
DB 265 --AKVIVFSSGPDLEPLIKEIVRRNITGR--IWLASEAWASSSLIAMPEYFHVVGTTIG 320
QY 107 LQL 109
DB 321 FGL 323

Search completed: November 1, 2001, 16:27:54
Job time: 174 sec
